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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 20, 2006, 19:48:48 ; Search time 3017 Seconds
(without alignments)

8017.612 Million cell updates/sec

Title: US-10-327-713-267

Perfect score: 468

Sequence: 1 gactgagtcgtggccatagg...ngcacacccgcctatgg 468

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqB, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: Genbank:*
2: gb_ba:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_sto:*
11: gb_sy:*
12: gb_un:*
13: gb_vl:*
14: gb_htg:*
15: gb_pl:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	415	88.7	2962	9 BC015301	BC015301 Mus musculus ATP-binding Cassette, sub-family B (MDR/TAP) member 8, mRNA (cDNA clone MGC:19206 IMAGE:4237894), complete cds.
2	378.2	80.8	2851	9 BC085781	BC085781 Rattus norvegicus ATP-binding Cassette, sub-family B (MDR/TAP) member 8, mRNA (cDNA clone MGC:19206 IMAGE:4237894), complete cds.
3	316	67.5	2309	8 AK22911	AK22911 Homo sapiens ATP-binding Cassette, sub-family B (MDR/TAP) member 8, mRNA (cDNA clone MGC:19206 IMAGE:4237894), complete cds.
4	316	67.5	2392	6 AX833134	AX833134 Sequence
5	316	67.5	2392	8 AK094636	AK094636 Homo sapiens ATP-binding Cassette, sub-family B (MDR/TAP) member 8, mRNA (cDNA clone MGC:19206 IMAGE:4237894), complete cds.
6	316	67.5	2417	6 C0717207	C0717207 Sequence
7	316	67.5	2487	6 BD156975	BD156975 Primer for sequencing
8	316	67.5	2487	6 AX87013	AX87013 Sequence
9	316	67.5	2487	8 AK002018	AK002018 Homo sapiens ATP-binding Cassette, sub-family B (MDR/TAP) member 8, mRNA (cDNA clone MGC:19206 IMAGE:4237894), complete cds.
10	316	67.5	5089	6 CQ850926	CQ850926 Sequence
11	316	67.5	5089	8 AK128129	AK128129 Homo sapiens ATP-binding Cassette, sub-family B (MDR/TAP) member 8, mRNA (cDNA clone MGC:19206 IMAGE:4237894), complete cds.
12	312.8	66.8	2417	8 AF047690	AF047690 Homo sapiens ATP-binding Cassette, sub-family B (MDR/TAP) member 8, mRNA (cDNA clone MGC:19206 IMAGE:4237894), complete cds.
13	302.4	64.6	2383	6 BD160664	BD160664 Primer for sequencing
14	302.4	64.6	2383	6 AX884014	AX884014 Sequence
15	302.4	64.6	2383	8 AK02401	AK02401 Homo sapiens ATP-binding Cassette, sub-family B (MDR/TAP) member 8, mRNA (cDNA clone MGC:19206 IMAGE:4237894), complete cds.
16	221	49.4	2199	8 AK094005	AK094005 Homo sapiens ATP-binding Cassette, sub-family B (MDR/TAP) member 8, mRNA (cDNA clone MGC:19206 IMAGE:4237894), complete cds.
17	186.2	39.8	744	6 BD150403	BD150403 Primer for sequencing
18	186.2	39.8	744	6 AX870341	AX870341 Sequence

ALIGNMENTS

RESULT	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
1	BC015301	BC015301 Mus musculus ATP-binding Cassette, sub-family B (MDR/TAP) member 8, mRNA (cDNA clone MGC:19206 IMAGE:4237894), complete cds.	BC015301	1	GT:1592975B	MGC.	Mus musculus (house mouse)
2	BC085781	BC085781 Rattus norvegicus ATP-binding Cassette, sub-family B (MDR/TAP) member 8, mRNA (cDNA clone MGC:19206 IMAGE:4237894), complete cds.	BC085781	1	GT:1592975B	MGC.	Rattus norvegicus
3	AK22911	AK22911 Homo sapiens ATP-binding Cassette, sub-family B (MDR/TAP) member 8, mRNA (cDNA clone MGC:19206 IMAGE:4237894), complete cds.	AK22911	1	GT:1592975B	MGC.	Homo sapiens
4	AX833134	AX833134 Sequence	AX833134	1	GT:1592975B	MGC.	-
5	AK094636	AK094636 Homo sapiens ATP-binding Cassette, sub-family B (MDR/TAP) member 8, mRNA (cDNA clone MGC:19206 IMAGE:4237894), complete cds.	AK094636	1	GT:1592975B	MGC.	Homo sapiens
6	C0717207	C0717207 Sequence	C0717207	1	GT:1592975B	MGC.	-
7	BD156975	BD156975 Primer for sequencing	BD156975	1	GT:1592975B	MGC.	-
8	AX87013	AX87013 Sequence	AX87013	1	GT:1592975B	MGC.	-
9	AK002018	AK002018 Homo sapiens ATP-binding Cassette, sub-family B (MDR/TAP) member 8, mRNA (cDNA clone MGC:19206 IMAGE:4237894), complete cds.	AK002018	1	GT:1592975B	MGC.	Homo sapiens
10	CQ850926	CQ850926 Sequence	CQ850926	1	GT:1592975B	MGC.	-
11	AK128129	AK128129 Homo sapiens ATP-binding Cassette, sub-family B (MDR/TAP) member 8, mRNA (cDNA clone MGC:19206 IMAGE:4237894), complete cds.	AK128129	1	GT:1592975B	MGC.	Homo sapiens
12	AF047690	AF047690 Homo sapiens ATP-binding Cassette, sub-family B (MDR/TAP) member 8, mRNA (cDNA clone MGC:19206 IMAGE:4237894), complete cds.	AF047690	1	GT:1592975B	MGC.	Homo sapiens
13	BD160664	BD160664 Primer for sequencing	BD160664	1	GT:1592975B	MGC.	-
14	AX884014	AX884014 Sequence	AX884014	1	GT:1592975B	MGC.	-
15	AK02401	AK02401 Homo sapiens ATP-binding Cassette, sub-family B (MDR/TAP) member 8, mRNA (cDNA clone MGC:19206 IMAGE:4237894), complete cds.	AK02401	1	GT:1592975B	MGC.	Homo sapiens
16	BD150403	BD150403 Primer for sequencing	BD150403	1	GT:1592975B	MGC.	-
17	AX870341	AX870341 Sequence	AX870341	1	GT:1592975B	MGC.	-

CONSRM

TITLE: NIH MGC Project
JOURNAL: Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBLISHED: 12/47/93
REFERENCE: 2 (bases 1 to 2962)

AUTHORS:
CONSRM: NIH MGC Project
TITLE: Direct Submission

JOURNAL Submitted (01-OCT-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA
 REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 COMMENT Contact: MGC help desk
 Email: cgapbs-r@mail.nih.gov
 TISSUE Procurement: Jeffrey B. Green, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILINL)
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: <http://www-sigc.stanford.edu>
 Contact: (Dickson, Mark) mcg@paxil.stanford.edu
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL site: <http://image.lnl.gov>

This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 27753994. Location/Qualifiers

FEATURES

source

organism="Mus musculus"

/mol type="mRNA"

/strain="FVB/N"

/db_xref="Taxon:10090"

/clone="MGC:19206 IMAGE:4237994"

/tissue type="kidney, normal. 5 month old male mouse."

/clone_id="NCI_CGAP_Kid14"

/lab_host="DHL0B"

/notes="vector: PCMV-SPORT6"

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/gene="Abcb8"

/db_xref="GeneID:74610"

341..2494

/genes="Abcb8"

/codon_start=1

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member 8"

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/db_xref="Generated:74610"

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/ab_xref="MGI:1351667"

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RQDLAHPDAKTTGQVSLRQSLTVDPERKSPKLVSQGLUSCTOTVLSLMSLSPRL

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RGSITFONVNTSYSPCPGRHSLVPLKPSKGOKRQVLFYRPFYD

BAGSITLGDHDLTLPMSWQGQVIGFISORPVFAFTTMINIFPGKUDASDEEVYTA

ARENAHEFISSPDQGYSTWVGRTLSQGOKRLATRALQTOVWLDETSAL

DABSERVYORALDRASAGRTVLTVAHLSTWRAMHSITWVANGVCAQATHBELLKG

GLYSELIRROTLDSLASLSTPPAEPEDPKSCQSA"

ORIGIN

Query Match

Best Local Similarity

91.9%

Score 415;

DB 9;

length 2962;

Matches 429;

Conservative

0;

Mismatches

37;

Indels

1;

Caps

1;

Reference

2

QY

2

ACTGAGCTGGCCCTAGGTGCGGCACTAGTGATGTCAGATGCCCTTGCTCTGGCCAG

61

Db

740

ATTTGGCTGGCCCTAGGTGCGGCACTAGTGATGTCAGATGCCCTTGCTCTGGCCAG

799

QY

62

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121

Db

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CTGGTGGAGATGTCGCCAACATACAGGGACCATGCGGAGTTTGCTCTGGATGTC

859

QY

122

CONAGCTCAGNCANCCTGCTCTACTGAGACAGTGAGCTGAGTCACTTGA

181

JOURNAL

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

PUBLISHED

12477932

REFERENCE

2

(bases 1 to 2851)

AUTHORS

NIH MGC Project

COMTRM

Direct Submission

Submitted (01-NOV-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA

REMARK

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Howard Jacobs

CDNA Library Preparation: Express Genomics

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILINL)

JOURNAL Submitted (01-OCT-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA
 REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 COMMENT Contact: MGC help desk
 Email: cgapbs-r@mail.nih.gov

TISSUE Procurement: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILINL)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305

Web site: <http://www-sigc.stanford.edu>

Contact: (Dickson, Mark) mcg@paxil.stanford.edu

Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL site: <http://image.lnl.gov>

This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 27753994. Location/Qualifiers

Db 860 CGTAACCTCACGGTCAGCTCTCTACTCTACGGTGTAGGAGCTGACCTTGG 919

QY 182 TACCTAGTGTAGCTGCTCCACATGNNGANCATGGCTAGNACATGGAAAGCCCT 241

Db 920 TACCTAGTGTAGCTGCTCCACATGGTGTAGGAGCTGACCTTGGAAAGCCCT 979

QY 242 TTGAGCTCTGCTCGGGAGACATTGCTTNTTGATGCCAAAAGACAGGGAGCGT 301

Db 980 TTGAGCTCTGCTCGGGAGACATTGCTTNTTGATGCCAAAAGACAGGGAGCGT 1038

QY 302 AGTGAATGGCTGACTGATGATGATGAGTGGCTTCAAGTCACTTCAGTTGCAATTN 361

Db 1039 AGTGAATGGCTGACTGATGATGAGTGGCTTCAAGTCACTTCAGTTGCAATTN 1098

QY 362 CCAGGAGCTGAGCTGAGCTGAGTGGCTTCAAGTCACTTCAGTTGCAATTN 421

Db 1099 CCAGGAGCTGAGCTGAGCTGAGTGGCTTCAAGTCACTTCAGTTGCAATTN 1158

QY 422 CCCTGCTTACCTGATGCTGGCTGCTGAGCAGCTGATGTTGGCTGCTGCTATGTC 468

Db 1159 CCCTGCTTACCTGATGCTGGCTGCTGTCACCGGCCCTCATGG 1205

		TITLE		Masuho,Y.
		JOURNAL		Full-length cDNA sequences
		PATENT		EP 1347046-A 258 24-SPB-2003;
FEATURES		Research Association for Biotechnology (JP)		
source		Location/Qualifiers		
ORIGIN		1..2392		/organism="Homo sapiens"
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Db		472 GTGCTGACCTTGTGGCGACTCTGGAATGAGCTTCCCTGCTCGGGCGAGTC 531		
QY		65 GTGAGAGATGTGGCCAAAGTAGACAGGAGGACACATGGGAGANTCCTGTTGANTCCGN 124		
Db		532 GTGAGAGTGTGGCCAAAGTAGACAGGAGGACACATGGGAGANTCCTGTTGANTCCGN 591		
QY		125 AAAGCTCAGNCANCAGCTCTACTGAGNACAGAGTTCAGGAGACTGTGACCTTNGATAC 184		
Db		592 AATCTCAGCACCCACCTCTTATCTCTATGTTGTCCAGGAACTGTGACCTTCGGTAC 651		
QY		185 CTAGTGCTGTGTCACATTGNGANCATGGCTGAGCATGAGCCCTTTC 244		
Db		652 CTTGGTGCCTGCTTCCAGTGTGGCGAGCAGTCAGTGGCTGAGCCCTTC 711		
QY		245 AGCTCCCTGCTGGGAGAACATGCTTNTTGTGTCAAAGAACAGGGCAGGAGTAGT 304		
Db		712 ACTTCCCCTGCTGGAGAACATCACCTTCTTGTGTCAAAGAACAGGGCAGC-TGGT 770		
QY		305 GAGTCGCTGTGACTACTGATGTCAGGATTCAGGATCTTGTGAGCTTGTGAGCTTGTGAC 364		
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QY		365 GGGACTGNGCACTGTGAGGCCAGGTGATGGCTGGAGGAGCCCTTCCC 424		
Db		831 GGAGCTGCGAAGCTGCAACCCAGTGGAGCTGCTGCTGCTGAC 890		
QY		425 TGGCTTACCTGTGCTGGCTGCTGAGGATGAGCTTGTGAGCTTGTGAGCTTGTGAC 468		
Db		891 AGCCCTCAGCTGCTGATGGTGG3CCACACCAGCCCTGATGG 934		
RESULT 4		AK094635		
LOCUS		AK094636		
DEFINITION		AK094636		
VERSION		AK094636		
SOURCE		AK094636..1 GI:21753734		
ORGANISM		Homo sapiens		
REFERENCE		Homo sapiens		
AUTHORS		Bukaruya, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Eutheriontognires; Primates; Catarrhini; Hominidae; Homo.		
ACCESSION		Ota,T., Suzuki,Y., Nishikawa,T., Otsuki,T., Sugiyama,T., Irie,R., Wakamatsu,A., Hayashi,K., Sato,H., Nagai,K., Kimura,K., Makita,H., Sekine,M., Ohayashi,M., Nishi,T., Shibahara,T., Tanaka,T., Ishii,S., Yamamoto,J., Saito,M., Isomoto,Y., Nakamura,Y., Nagahashi,K., Murakami,K., Yasuda,T., Iwayanagi,T., Waga,Shimamura,M., Shiratori,A., Sudo,H., Hosoi,T., Kaku,Y., Kodaira,H., Konno,H., Sugawara,M., Takahashi,M., Kanda,K., Yokoi,T., Furuya,T., Kikkawa,E., Omura,Y., Abe,K., Kamiyama,K., Kataoka,N., Sato,K., Tanikawa,M., Yamazaki,M., Ninomiya,K., Isibashi,T., Yamashita,H., Murakawa,K., Fujimori,K., Tanai,H., Kimata,M., Watanabe,M., Hiraoka,S., Chiba,Y., Ishida,S., Ono,Y., Takiguchi,S., Watanabe,S.,		
REFERENCE		Isegai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S., Yamamoto,J.I., Isomoto,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R., Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahashi,K. and		
AUTHORS				

				AGRTVVIARLSTVRGANICIVVMADGRVWEAGTHEELLKGGLYAEILRQALDAPR TAAPPKPKPBPSPRSHQKS"
Yosida,M., Hotuta,T., Kusano,J., Kanehori,K., Takahashi-Fujii,A., Hara,H., Tannase,T., Nomura,Y., Togoya,S., Konai,P., Hara,R., Takemoto,K., Arita,M., Imose,N., Musashino,K., Yuuki,H., Oshima,A., Sasaki,N., Aotsuka,S., Yoshikawa,Y., Matsunawa,H., Ichihara,T., Shiohata,N., Sano,S., Moriya,S., Momiyama,H., Sakoh,N., Takami,S., Terashima,Y., Suzuki,O., Nakagawa,S., Senoh,A., Mizoguchi,H., Goto,Y., Shimizu,F., Wakobe,H., Hishigaki,H., Watanabe,T., Sugiyama,A., Takekoto,M., Kawakami,B., Yamazaki,M., Watanabe,K., Kumagai,A., Itakura,S., Fukuzumi,Y., Fujimori,Y., Komiyama,M., Tashiro,H., Tanigami,A., Fujiwara,T., Ono,T., Yamada,K., Fujii,Y., Ozaki,K., Hirao,M., Ohmori,Y., Kawabata,A., Hikiji,I., Kobatake,N., Inagaki,H., Ikeda,Y., Okamoto,S., Okitani,R., Kawakami,T., Noguchi,S., Itoh,T., Shigeta,K., Senba,T., Matsumura,K., Nakajima,Y., Mizuno,T., Morinda,M., Sabaki,M., Togashi,T., Oyama,M., Hata,H., Wattanabe,M., Komatsu,T., Mizushima,Sugano,J., Sakoh,T., Shiba,Y., Takahashi,Y., Nakagawa,K., Okumura,K., Nagase,T., Nomura,N., Kikuchi,H., Masuno,Y., Yamashita,R., Nakai,K., Yada,T., Nakamura,Y., Ohara,O., Isogai,T. and Sugano,S.				
TITLE	Complete sequencing and characterization of 21,243 full-length human cDNAs			
JOURNAL	Nat. Genet.	36 (1), 40-45 (2004)		
PUBLISHED	14702039			
REFERENCE				
AUTHORS				
2	Ninomiya,K., Wagatsuma,M., Kanda,K., Kondo,H., Yokoi,T., Kodaira,H., Furuya,T., Takahashi,M., Kitkawa,E., Omura,Y., Abe,K., Kamihara,K., Kubota,N., Sato,K., Tanikawa,M., Yamazaki,M., Sugiyama,T., Irie,R., Otsubi,T., Sato,H., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hie,Y., Saito,K., Nishikubo,T., Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Murakawa,K., Kaneko,I., Takahashi-Fujii,A., Osahime,A., Sugiyama,A., Kawachi,B., Suzuki,Y., Sugano,S., Nagahori,K., Masuno,Y., Nagai,K. and Isogai,T.			
TITLE	NEO human cDNA sequencing project			
JOURNAL	Unpublished			
REFERENCE	3 (bases 1 to 2392)			
AUTHORS	Isogai,T. and Yamamoto,J.			
TITLE	Direct Submission			
JOURNAL	Submitted (04-JUL-2002) Takao Isogai, PLJ Project (HRI Team); 2-6-7 Kazusa-Kamateru, Kisarazu, Chiba 292-0812, Japan			
COMMENT	Economy; Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB. Location: HRI and RAB.			
FEATURES				
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ORIGIN				
AUTHORS	Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.			
REFERENCE	Kits, such as nucleic acid arrays, comprising a majority of humanoxons or transcripts, for detecting expression and other uses thereof			
JOURNAL	Patent: WO 02058579-A 3141 06-SEP-2002; PE Corporation (NY) (US)			
FEATURES				
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Query Match	67.5%; Score 316; DB 6; Length 2417;			
Best Local Similarity	78.9%; Pred. No. 4-4e-69;			
Matches	366; Conservative 0; Mismatches 97; Indels 1; Gaps 1;			
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				ENIRFGKLEASDEEVYTAAREANAHFTSPEGINVWGRGFTLISGGOKORIAR
				ALIKOPTVILDEATSAALDAESERVOBALDRASAGRTVILVIAHKUSTVROAHCI.VVM
				ADGRVWEAGTHEBLKKGLYVABLRRQALDAAPRTAAPPKPKPGRSPSHOKS"
				ORIGIN
Query Match	67.5%	Score 316; DB 6;	Length 2487;	
Best Local Similarity	78.9%	Pred. No. 4.4e-69;	Indels 1;	Gaps 1;
Matches	366;	Conservative 0;	Mismatches 97;	
Qy	5 GAGCTGGCCTAGGTGGCCACTGTGAATGTCAGATCCCTGCTGGCCAGCTG 64			
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DEFINITION	Homo Sapiens cDNA FLJ11156 fis, clone PLACE1006956,	weakly similar		PRI 30-JAN-2004
ACCESSION	to ATP-DEPENDENT PERMEASE NDII.			CDS
VERSION	AK002018			
KEYWORDS	AK002018.1 GI:7023645			
SOURCE	Organism Homo Sapiens (human)			
ORGANISM	Homo Sapiens			
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FEATURES				
source	Isogai, T. and Otsuki, T. Direct Submission Submitted (16-FEB-2000) Takao Isogai, Helix Research Institute, Genomics Laboratory, 1-32-2 Yana, Kibarzu, Chiba 292-0812, Japan (E-mail:genomests@hri.co.jp); Tel:81-438-52-3975; Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing; Research Association for Biotechnology; cDNA library construction; 5'- and 3'-end one pass sequencing and clone selection; Helix Research Institute (Supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.			
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Db	523 GTGCTGGCCTTGGTGGCGACTCTGATGAGTACAGATGCCCTGCTGGCCAGCTG 582			

QY	65	GTTGAGAGATGTGCCAAGTAGACGGAGGACCATGGAGNTNGTNTGANTCCGN	124	Db	790	CTGGTGTCTGTGTCACAGTGGGAGGCATGGCTGACATGGGGAGGCCCTTC	849
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Db	643	ATCTCTAGCACACCACTGCTATTCTCTATGTCAGCCAGGCTCGGTAC	702	QY	305	GAGTGCTGACTACTGATGTGAGAATCAAGCAGTGGCTGAGCTTCGGTAC	364
QY	185	CTAGTCGCTGCTCCACATTGNGNANCNCITGGCATGACATCGGAAGACCTTTC	244	Db	909	GAGCCGCTTGAACACTGACTGAGGTTAAGTCATCTCAGCTGTGTCATCCCA	968
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QY	245	AGCTCCCCTGCTCGGCAAGAATGTTINTTGTGCCAAGAACAGGGAGGTTA	304	Db	969	GGGCTTGAGCTGACCCAGGGTGGCTGCTGCTGCTGCTGCTGCTGAC	1028
Db	763	AGTCCTGCTGCTGACAGAACATCACTTCTTGAGCCAAATAAGACGGCAGG-TGT	821	QY	425	TGCGCTTACCTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	468
QY	305	GAGTCGCTGACTACTGATGTGCAAGAATGATTAGGATCTNAAGCTGCTGATNTCCA	364	Db	1029	ACGCCTCACCGCTGCTGATGGTGGCTGACACCAACGCCCTGATGG	1072
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Db	882	AGGCTCTGGAGACTGACCAAGGCTGAGGCTGCTGCTGCTGCTGCTGAC	941				
QY	425	TGCGCTTACCTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	468				
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DEFINITION	Sequence 1395 from Patent EP1447413.						
ACCESSION	CQ850926						
VERSION	CQ850926.1						
KEYWORDS							
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REFERENCE							
AUTHORS	Isegai,T., Yamamoto,J., Nishikawa,T., Isono,Y., Sugiyama,T.,						
TITLE	Full-length human cDNA						
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Db	730	ATCTCTAGCACACCACTGCTTATGTCAGCCAGGACTGACTGCTCGGTAC	789				
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DEFINITION	Homo sapiens cDNA FLJ46250 fis, clone TESTI4021569, moderately similar to ATP-binding cassette, sub-family B, member 8,						
ACCESSION	AK128129						
VERSION	AK128129.1						
KEYWORDS	AK128129.1 GI:34535347						
SOURCE	oligo capping; fis (full insert sequence).						
ORGANISM	Homo sapiens (human)						
REFERENCE							
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo.						
TITLE							
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AUTHORS	Ota,T., Nakagawa,S., Senoh,A., Mizuguchi,H., Inagaki,H., Isegai,T., Sugiyama,T., Nakashita,H., Kawai-Hiro,Y., Saito,H., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hiro,Y., Saito,K., Nakamura,Y., Sekine,M., Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Takahashi-Fujii,A., Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S., Nagahiri,K., Masuno,Y., Nagai,K. and Isegai,T.						
TITLE	Unpublished						
JOURNAL	2 (bases 1 to 5089)						
REFERENCE	Isegai,T. and Yamamoto,J.						
AUTHORS	Direct Submission						
TITLE							
JOURNAL							
COMMENT	Submitted (15 JULY-2003) Takao Isegai, FLJ Project (HRI Team); 2-6-7 (B-mail:genomics@hri.co.jp; Tel: 81-38-52-3975, Fax: 81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert Sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5' - 3' end one pass Sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: Reverse Proteomics Research Institute, HRI and RAB.						
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ORIGIN

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	VERSION	AF047690.1	G1:4321406			
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	AUTHORS	Hogue, D.L., Liu, L. and Ling, V.				
	TITLE	Identification and characterization of a mammalian mitochondrial ATP-binding cassette membrane protein				
	JOURNAL	J. Mol. Biol. 285 (1), 379-389 (1999)				
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	AUTHORS	Hogue, D., Liu, L. and Ling, V.				
	TITLE	Direct Submission				
	JOURNAL	Submitted (12-FEB-1998) BC Cancer Research Centre, 600 West 10th Avenue, Vancouver, BC V5Z 4L3, Canada				
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LOCUS	BD160664			
DEFINITION	Primer for synthesizing full-length cDNA and use thereof.			
ACCESSION	BD160664			
VERSION	BD160664.1			
KEYWORDS	GI:2786422			
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	Hominidae; Homo.			

REFERENCE		ORGANISM		
AUTHORS	Otta, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J., Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T.	Bukuyota, Metzoco, Chondata, Craniata, Vertebrata, Euteleostomi, Mammalia, Benthontoglires, Primates, Catarrhini, Hominidae, Homo.		
TITLE	Primer for synthesizing full-length cDNA and use thereof	PRIMER FOR SYNTHESIZING FULL-LENGTH cDNA AND THEIR USE		
JOURNAL	HELIX RESEARCH INSTITUTE	PATENT	EP 1074617/2001, PCT/JP2002/09136-A, 15507, 09-JUL-2002;	
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Db	365 GGAACTGNCAGCTGNGACCAGGTTATGTGACCTGAGNCCTCTGNTATGTCGCC 424 778 GGAGCTGCGAGAGCACCAGGTGCAAGCTGCTGCTGCTGCTGCTGCTGAC 837	PI		
Qy	425 TCGCTTACCTGAGTGTGCTGATGAGGCGCACACAGGCCATGG 468 838 ACCGCTTCAGCTGCTGCTGATGAGGCGCACACAGGCCATGG 881	PI		
RESULT 14	AX884014 AX884014 Sequence 18919 from Patent EP1074617. 2383 bp DNA linear PAT 17-DEC-2003	PI		
LOCUS	DEFINITION	ACCESSION	VERSION	
KEYWORDS	Homo sapiens (human)	AX884014.1 GI:40038915		
RESULT 15	AX884014 AX884014 2383 bp mRNA linear PRI 30-JAN-2004	PI		
DEFINITION	Hom sapiens cDNA FLJ14339 f.8, clone SKMC1000013, highly similar	ACCESSION	AK024401	
SOURCE		LOCUS	AK024401	

ACCESSION	to Homo sapiens ATP-binding cassette protein M-ASCL mRNA, nuclear gene encoding mitochondrial protein.
VERSION	AK024401.1
SOURCE	AK024401.1 GI:10436780 oligo capping; fts (full insert sequence).
ORGANISM	Homo sapiens (human)
FEATURES	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R., Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H., Sekine, M., Obayashi, M., Nishi, T., Shibakawa, T., Tanaka, M., Nakamura, Y., Ishii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y., Nagahara, K., Murakami, K., Yasuda, T., Iwayanagi, T., Wagatsuma, M., Shiratori, A., Sudo, H., Hobori, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Furuya, T., Kikuchi, E., Omura, Y., Abe, K., Kamiyama, K., Kataoka, N., Sato, K., Tanikawa, M., Yamazaki, M., Ninomiya, K., Ishibashi, T., Yamashita, H., Murakawa, K., Fujimori, K., Tani, H., Kimata, M., Watanabe, M., Hirao, S., Chiba, Y., Ishida, S., Ono, I., Takiguchi, S., Watanabe, S., Yosida, M., Hotoda, T., Kubano, J., Kanehori, K., Takahashi, F., Fujii, A., Hara, H., Tanase, T., Nomura, Y., Togita, S., Komai, F., Hara, H., Takeuchi, K., Arita, M., Imobe, N., Murashimo, K., Yuuki, H., Oshima, A., Sasaki, N., Aotsuka, S., Yoshihikawa, Y., Matsunawa, H., Ichihara, T., Shiohata, N., Sano, S., Moriya, S., Moniyya, H., Satoh, N., Terashima, Y., Suzuki, O., Nakagawa, S., Senoh, A., Mizoguchi, H., Goto, Y., Shimizu, F., Wakebe, H., Hisigaki, H., Watanabe, M., Watanabe, K., Sugiyama, A., Takekumo, M., Kawakami, B., Yamazaki, M., Watanabe, K., Kumada, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiya, M., Tashiro, H., Tanigami, A., Fujiwara, T., Ono, T., Yamada, K., Fujii, Y., Ozaki, K., Hidai, M., Ohmori, Y., Kawabata, A., Hikiji, T., Kobatake, N., Inagaki, H., Ikemoto, Y., Okamoto, S., Okiyama, R., Kawakami, T., Noguchi, S., Itoh, T., Shigeta, K., Seiba, T., Matsumura, K., Nakajima, Y., Mizuno, T., Morinaga, M., Sasaki, M., Topashi, T., Oyama, M., Hata, H., Watanabe, M., Komatsu, T., Mizushima-Sugano, J., Satoh, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K., Nagase, T., Nomura, N., Kikuchi, H., Masuda, Y., Yamashita, R., Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isogai, T., and Sugano, S. Complete sequencing and characterization of 21,243 full-length human cDNAs
JOURNAL	Nat. Genet. 36 (1), 40-45 (2004)
PUBLISHED	14702039
REFERENCE	2 Isogai, T., Ota, T., Hayashi, K., Sugiyama, T., Otsuki, T., Suzuki, Y., Nishikawa, T., Nagai, K., Saito, H., Sugano, S., Shiratori, A., Sudo, H., Nagatsuma, M., Hobo, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Chiba, Y., Ishida, S., Murakawa, K., Ono, Y., Takiguchi, S., Watanabe, S., Kimura, K., Murakami, K., Ishii, S., Kawai, Y., Saito, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagahara, K., Masuda, Y., Ninomiya, K. and Iwayanagi, T. NEDO human cDNA sequencing project Unpublished 3 (bases 1 to 2383) Isogai, T. and Otsuki, T. TITLE Direct Submission JOURNAL Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute, Genomics Laboratory, 1532-3 Yana, Kiarazaru, Chiba 282-0812, Japan (E-mail: genomics@shri.co.jp; Tel: 81-438-52-3975, Fax: 81-438-52-3986) COMMENT International Trade and Industry of Japan; cDNA full insert sequencing; Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing and clone selection; Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of virology, Institute of Medical Science, University of Tokyo.
FEATURES	Location/Qualifiers /cell_line="SK-N-MC" /clone="cloning vector: pMB18SFL3" /note="cloning vector: pMB18SFL3" /note="compared to AF047690 and AC010973. 4" /replace="g"
ORIGIN	Query Match 64.6%; Score 302.4; DB 8; Length 2383; Best Local Similarity 78.4%; Pred No. 1.2e-65; Matches 364; Conservative 0; Mismatches 98; Indels 2; Gaps 2;
5	GAGCTGGCTTAGGTGGCGACTAGTGAATGAGATCCCTCTCCCTGGCGAGCTG
QY	420 GTGCCTGGCTTGGGGCGACTCTGATGAGATCCCTCTCCCTGGCGAGCTG
Db	479 GTAGGGGTCTGGCCAGTGACAGACAGGGGTTATGAGCTGAGTCAG
QY	539 ATCTCAGCACTCACCTGCTATCTCTATGGTGTCCAGGGACTGTCACCTTCGAGT
Db	598 124 GTGGAGATGTCGCCAGAACAGACATGGGGNTGNTGANTCCGN
QY	659 184 AGCTCTGCTGGTCCACATTGGANGANCNTGGCATGAGATGGGAAGGCCRTTC
Db	659 244 CTAGCTGTGGTCCACATTGGANGANCNTGGCATGAGATGGGAAGGCCRTTC
QY	718 658 304 AGCTCTGCTGGTCCACATTGGANGANCNTGGCATGAGATGGGAAGGCCRTTC
Db	718 777 365 365 GAGACTGCGACTGACCCGGTTAGTCATCTCAAGTGTCTCCCA
QY	778 837 424 778 GGGCTGGAGCTGCACTGGTGGAGCCCTGCTGTCCTGTCATGTCGAC
Db	425 425 TGGCTTACCGTGTGGTGGNNNACACCCGGCCCTCTGG
QY	838 881 AGCTCTACGGCTGGCTGATGTTGGCCACCGCCCTGATGG
Db	

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 20, 2006, 16:27:08 ; Search time 470 Seconds

(without alignments)
6363.332 Million cell updates/sec

Title: US-10-327-713-267

Perfect score: 468

Sequence: 1 gactgagctggcccttaaggtagtgg.....ngacacaccgcgcctatgg 468

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

listing first 45 summaries

Database :

N_Geneseq_21:*

1: geneseq1900:*

2: geneseq1900:*

3: geneseq2000:*

4: geneseq2001as:*

5: geneseq2001bs:*

6: geneseq2002as:*

7: geneseq2002bs:*

8: geneseq2003as:*

9: geneseq2003bs:*

10: geneseq2003cb:*

11: geneseq2003db:*

12: geneseq2004as:*

13: geneseq2004bs:*

14: geneseq2005bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description	ALIGMENTS
1	315	67.5	2392 11 ADM01573	RESULT 1	
2	316	67.5	2417 6 AAK34932	ID ADW01573 standard; cDNA; 2392 BP.	
3	316	67.5	2487 4 AAH14983	ID ADW01573;	
4	315	67.5	2562 3 ADD0603	XX DT 20-MAY-2004 (first entry)	
5	315	67.5	3212 13 ACN41862	XX DB Human cDNA of the invention SEQ ID NO:258.	
6	315	67.5	5089 13 ADR07889	XX KW 88; Gene; human; gene therapy; diagnostic marker; pharmaceutical.	
7	315	67.3	1211 3 ACT7613	XX OS Homo sapiens.	
8	302.4	64.6	2383 4 AAK18672	XX PN EP1347046-A1.	
9	277.6	59.3	1251 3 AAA62022	XX PD 24-SBP-2003.	
10	277.6	59.3	1617 3 AAA62032	XX PP 12-APR-2002; 2002JP-00008400.	
11	230	49.1	2317 13 ACN41861	XX PR 22-MAR-2002; 2002JP-00137785.	
12	219.6	46.9	1805 6 ABL18954	PA (REAS-) RBS ASSOC BIOTECHNOLOGY.	
13	206.8	44.2	449 9 ACH43729	XX PI Isogai T, Sugiyama T, Otsuka T, Wakamatsu A, Sato H, Ishii S; Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I; Seki N, Yoshikawa T, Otsuka M, Nagahashi K, Masuno Y;	
14	206.8	44.2	1023 3 AAR22411	XX PT New Polynucleotides and polypeptides are useful in gene therapy, for developing a diagnostic marker or medicines for regulating their expression and activity, or as a target of gene therapy.	
15	186.2	39.8	744 4 AAR08411	PT New Polynucleotides and polypeptides are useful in gene therapy, for developing a diagnostic marker or medicines for regulating their expression and activity, or as a target of gene therapy.	
16	127.8	27.3	423 9 AAF92351	CC The invention relates to a novel human polynucleotide and the encoded polypeptide. A polynucleotide of the invention may have a use in gene therapy. An oligonucleotide of the invention ADW06205-ADW06773 is useful as a primer for synthesizing the polynucleotide or as a probe for detecting the polynucleotide. The polynucleotides ADW01316-ADW03758 are	
17	117.6	25.1	425 9 ACH47047	CC	
18	93	19.9	2379 4 ABL03511	CC	
19	93	19.9	4940 4 ABL03510	CC	

Aah07823 Human cDN
Aal10675 Human rep
Aaa40273 DNA encod
Adj03268 Human pro
Ab190156 Human pol
Ac167748 M. xanthu
Act44704 Bacterial
Ac16746 M. xanthu
Act75564 Human ORP
Ac167610 M. xanthu
Adt44685 Bacterial
Ac16739 M. xanthu
Abv30083 Human pro
Abv45565 Human pro
Adq39136 Human SNP
Adt45448 Human vas
Adq07183 Human tum
Adq84906 Human tum
Abx76157 Lung canc
Adq18965 Human sof
Ado05813 Novel bro
Ado05806 Cyclin-de
Adq39138 Human SNP
Abk64501 Human ben
Adq23327 Human sof
Ach12996 Human adu

useful in gene therapy, for developing a diagnostic marker or medicine for regulating their expression and activity, or as a target of gene therapy. The proteins ADM03759-ADM0201 encoded by the polynucleotides are useful as pharmaceutical agents. The present sequence represents a cDNA sequence of the invention.

Sequence 2392 BP; 413 A; 766 C; 747 G; 466 T; 0 U; 0 Other;

```

Query Match 67.9%; Score 316; DB 11; Length 2392;
Best Local Similarity 67.9%; Pred. No. 9; Ge-811;
Matches 366; Conservative 0; Mismatches 97; Indels 1; Gaps 1

```

(GEMV) GENETICS INST INC.
Wong GG, Clark HF, Pechtel K, Agostino MJ, Howes SH, Renick RJ;
Guilkota, K, Graham JR;
WPI; 2002-179323/23.

Six hundred and twenty five polynucleotides derived from a variety of human tissue sources which encode secreted proteins, useful for treating immune deficiencies and disorders such as autoimmune disorders.

Db	872	ACGCCCTCACGCTGCTGATGGGCCACCCAGCCTGTGAG 915	Db	523	GTCGCTGCCTTGGGGCGGGACTCGTAAGATCCCGCTGCTGGCCAGCTG 582
RESULT 3			QY	65	GTTGGAGATGGTGCCGAGTAGTACAGAGGACCATGGGAGNTCTGNTGANTCCGN 124
AAH14983	ID	AAH14983 standard; cDNA; 2487 BP.	QY	583	GTAGAGCTCGTGGCCAGTAGACAGGACCACTGGAGGAGTTCACTGAGTCAGTCAG 642
XX	AC	AAH14983;	QY	125	AAGCTCANCAGNCANCTGCTCTACTGAGACAGTGAGGAGACTGAGTCAGTCAGTCAG 184
XX	DT	26-JUN-2001 (first entry)	Db	643	AATCTCGACCCACCTGCTCTATGGTCAGGAGCTGCTGACCTTCGGGTAC 702
XX	DR	Human cDNA sequence SEQ ID NO:12918.	QY	185	CTAGTGCTGCTCCACATTGNGANNCATGGCATGACATGCGAAGCCATTTC 244
XX	KW	Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.	Db	703	CCTGGCTGCTCCACCTGCTCTATGGTCAGGAGCTGCTGACCTTCGGGTAC 762
XX	OS	Homo sapiens.	QY	245	AGCTCCCTGCTCGGAAGACATGCTTNTGATGCCAAAAGAGCAGGGAGCTGT 304
XX	PN	(HBLI-) HELIX RES INST.	Db	763	ACCTCCCTGCTCGGAAGACATGCTTNTGATGCCAAAAGAGCAGGGAGCTGT 821
XX	PD	EP1074617-A2.	QY	305	GAGTCCTGCTGACTCTGCAAGATTCAGGCTTCCTTNAAGCTGTCATNTCCA 364
XX	PP	07-FEB-2001.	Db	822	GAGCCGCTGACATCTGCTCTGGGTTAGTCATCCCTCAAGCTGTCATCTCCA 881
XX	PR	28-JUL-2000; 2000EP-00116126.	QY	365	GAGACTCTGCTGCGGAAGACATGCTTNTGATGCCAAAAGAGCAGGGAGCTGT 424
XX	PR	29-JUL-1999; 99JP-00248936.	Db	882	GAGGCTCTGAGCTGCTGCCAGTGTGAGGCTCTGGTGTGTCATCTGAC 941
XX	PR	27-AUG-1999; 99JP-00300253.	QY	425	TGGCTTACCCCTGATGTTGGCTGGNNNNACACCCGGCTCATGG 468
XX	PR	11-JAN-2000; 2000JP-00118776.	Db	942	ACGCTTACGGCTCTGATGTTGGCTGACACCCGGCTGAG 985
XX	PR	02-MAY-2000; 2000JP-00183867.	QY		
XX	PR	09-JUN-2000; 2000JP-00241899.	DB		
PA		(HBLI-) HELIX RES INST.	XX		
XX	PI	Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;	XX		
XX	PI	Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;	XX		
XX	DR	WPI; 2001-318749/34.	XX		
XX	PT	Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.	XX		
XX	PT	Claim 8; SEQ ID NO 12918; 2537PP + Sequence Listing; English.	XX		
XX	PT	The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises:	XX		
CC	(a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprise at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the sequence and an oligonucleotide comprising a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH1842 represent human cDNA sequences; AAB2446 to AAB9589 represent human amino acid sequences; and AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention	XX			
CC	SQ	Sequence 2487 BP; 440 A; 788 C; 777 G; 482 T; 0 U; 0 Other;	XX		
CC	CC	Query Match Similarity 67.5%; Score 316; DB 4; Length 2487; Best Local Similarity 78.9%; Pred. No. 1e-80; Matches 365; Conservative 0; Mismatches 97; Indels 1; Gaps 1;	XX		
CC	CC	5 GAGCTGGCCTTAGGTCGGGACTACTGAAATGTCAGATCCCTTGCTCTGGCCAGCTG 64	XX		
CC	CC	(INCY-) INCYTR PHARM INC.	XX		
XX	Key	location/Qualifiers	XX		
XX	FT	79. .2235	XX		
XX	FT	*tag= a /product= "Membrane transport protein-4"	XX		
XX	FT	/WO20026245-A2.	XX		
XX	PP	11-MAY-2000.	XX		
XX	PP	04-NOV-1999; 99WO-US026048.	XX		
XX	PR	04-NOV-1998; 98US-0172255P.	XX		
XX	PR	24-NOV-1998; 98US-0172252P.	XX		
XX	PR	22-DEC-1998; 98US-0172214P.	XX		
XX	PR	26-FEB-1999; 99US-0121896P.	XX		
XX	PA	(INCY-) INCYTR PHARM INC.	XX		

PI Hillman JI; Yue H; Tang YT; Lal P; Corley NC; Guegler KJ;
 PI Baughn MR; Azimzai Y; Lu DAM;
 XX
 DR WPI; 2000-365576/31.
 DR P-PSDB; AAY71059.

PT Novel human membrane transport proteins useful for diagnosis, prevention and treatment of membrane transport disorders, immune/inflammatory disorders and cell proliferative disorders including cancer.
 PT
 XX
 PS Claim 9; Page 113-114; 136pp; English.

The present sequence is a cDNA encoding membrane transport protein, MTRP-4 from Incyte clone 2274390 isolated from human PROSNOM1 cDNA library. MTRP-4 shows homology to human ATP-binding cassette (ABC) transporter (GI 4321407), and schistosoma mansoni ABC family protein, SMDR1. It is expressed in reproductive, nervous, gastrointestinal and haemopoietic/immune tissues. The present sequence is useful in diagnosis, prevention and treatment of disorders related with increased or decreased expression of MTRP such as familial goitre, Mankes disease, diabetes, Parkinson's disease, depression, epilepsy, schizophrenia, immune/inflammatory disorders such as AIDS, Addison's disease, allergies, atherosclerosis, Graves disease, gout, Hashimoto's thyroiditis, viral, bacterial, fungal, parasitic, protozoal or helminthic infections and cell proliferative disorders such as cancer. Fragments of MTRP polynucleotides are useful as targets in microarrays. MTRP DNA is also useful for generating hybridisation probes useful in mapping genomic sequences and detecting differences in sequences among normal, carrier and affected individuals. It is also used for screening libraries of compounds in drug screening technique.

Sequence 2562 BP; 444 A; 824 C; 793 G; 501 T; 0 U; 0 Other;

Query Match 67.5%; Score 316; DB 3; Length 2562;
 Matches 366; Conservative 0; Mismatches 97; Indels 1; Gaps 1;

Qy 5 GAGCTGCCTTATGAGCAGCACTAGTGAATCGACATCCCTTGTCTCGGGCCAGTG 64
 Db 484 GTCGCTGGCTTATGGCGACACTCGTGTAAATCACAGATCCCTGCTGGCGAGCTG 543

SQ Sequence 2562 BP; 444 A; 824 C; 793 G; 501 T; 0 U; 0 Other;

Query Match 67.5%; Score 316; DB 3; Length 2562;
 Matches 366; Conservative 0; Mismatches 97; Indels 1; Gaps 1;

Qy 65 GCGAGATTCGCGCAAGTACAGGAGCACATCGGGAGTCAGTGTGTTGAGTCGGCG 124
 Db 544 GTGAGGGTGTGGCGCAAGTACAGGAGCACATCGGGAGTCAGTGTGTTGAGTCGGCG 603

Qy 125 AGACTCAGNCGNCANCTGCTCTACTAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTC 184
 Db 604 AACTCAGAACCACTCTTATCCCTATGGTCAGGAGCTGTGACTTCGGTAC 663

Qy 185 CTAGTGTGCTGCCATATTGNGANCNCTGGCATGNCATGGGAAAGGCCCTTTC 244
 Db 664 CTGGTGTGCTGCCAGCTTACGGCAAGCTGGGAGTCAGTCAGTCAGTCAGTCAGTC 723

Qy 245 AGCTCCGTGCTGCCAGACATTCGGTNTTGTGCAAAAAGCAGGCGAGCTACT 304
 Db 724 ASCTCCCTGCTGCCAGACATACCTCTTGTGCAAAAGCAGGCGAGCTACT 782

Qy 305 GACTCGCTGACTACTGATGTCAGAAGATTCAAGGCACTCTTAAAGTGTGATNCCA 364
 Db 783 GAGCGCTTGTGACACTGAGTCAGGAGTTTAAGTCATCTTCAGTTGATCTCCA 842

Qy 365 GAGACTCTGCGCTGACCGCTGTTGAGTCAGTCAGTCAGTCAGTCAGTCAGTC 424
 Db 843 GGGCTGCGGAAGCTGCACCCAGTGGCAGGGCTGCCTGTGTCATGTGAC 902

Qy 425 TGCCTTACCTGATGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTC 468
 Db 903 AGGCTCACTGCTGATGATGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTC 946

ID ACN41862 Standard; cDNA; 3212 BP.
 XX
 XX ACM41862;

AC DT 18-NOV-2004 (first entry)
 XX DS Human diagnostic and therapeutic polynucleotide SEQ ID NO:737.
 XX KW ss: gene; gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
 XX KW dithp.

XX OS Homo sapiens.
 XX PN WO2004023973-A2.
 XX PR 12-SBP-2002; 2002US-0410259P.
 XX PR 12-SBP-2002; 2002US-0410260P.

XX PA (INCY-) INCYTE CORP.

XX PI Schmidt JP; Wright RJ; Bruns CM; Marjanovic MM; Shen F; Elder JV;
 XX PI Harthorne TA; Suchotolski MT; Altius CM; Pletsch SJ; Mooney EM; Deleagean AM; Panesar IS; Barville SC; Reddy TP;
 XX PI Stevens KH; Blanchard JL; Panzer SK; Wang X; Au AP; Gertin EH;
 XX PI Peraulta CH; Anderson SJ; Rioux EA; Wu MC; Stuve LL; Lagace RB; Spiro PA; Stewart JA; Rioux EA; Wingeore J; Vitt UA; Kirton RS;
 XX PI Xu Y; Kuong M; Policky JL; Hurwitz BL; Ma Y; Jackson JL; Gietzen D;
 XX PI Patury S; Shi X; Suarez CJ;

XX DR WPI; 2004-329368/30.

XX DR P-PSDB; ABM83210.

XX PT New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or in gene mapping.

XX SQ Claim 1; Page: 190pp; English.

The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therapy. The human diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g., cell proliferative disorders, autoimmune/inflammatory disorder, developmental disorder, endocrine disorder, neurological disorders, gastrointestinal disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp molecules may also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline gene therapy. The present sequence represents a dithp polynucleotide of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm

XX Sequence 3212 BP; 565 A; 1056 C; 938 G; 653 T; 0 U; 0 Other;

Query Match 67.5%; Score 316; DB 13; Length 3212;
 Best Local Similarity 78.9%; Pred. No. 1..1e-80;
 Matches 366; Conservative 0; Mismatches 97; Indels 1; Gaps 1;

Qy 5 GAGCTGCCTTATGGCGACACTAGTCAGTCAGTCAGTCAGTCAGTCAGTC 64
 Db 538 GTCGCTGGCTTGGGGCGACACTCTGAGTCAGTCAGTCAGTCAGTCAGTCAGTC 597

RESULT 5
 ACN41862

QY 125 AAGCTCANCAGNCANCTGCTCTACTGNACAGAGTCAGGAACTTGACCTTNGATAC 184
 CC ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 658 AACTCAGCACCCACCTGCTTATCCCTATCTGCTGCTGAGCACTGTGACTTCGGTAC 717
 CC ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 185 CTAGTCTGTGCTGCCACATGCTTATCCCTATCTGCTGCTGAGCACTGTGACTTCGGTAC 244
 CC ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 718 CCGGTCTGTCTCCAGCTGTTGGAGGCGATGGCTTGAGCATGGCGAGGSCCCCTTC 777
 CC ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 245 AGCTCCCTGTCGGCGAGAGATAATGCTTNTTGTAGTCCAAAGAGCAGSCAGGTGT 304
 CC ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 778 AAGCTCCTGTCGGCGAGAGATAATGCTTNTTGTAGTCCAAAGAGCAGSCAGGTGT 836
 CC ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 305 GAGTCGCTGTACTACTATGTCAGAAGATTCAGGATCTTNAAGCTGTCATINCCA 364
 CC ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 837 GAGCCGTTAACACTGACGTCAGGTTAGTCATCTTCACCTGTGATCTCCCA 896
 CC ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 365 GAGACTGTGCACTGTGAGCTGAGCTGTTAGTGGAGGCTGAGCTGAGCTGAGCTG 424
 CC ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 897 GAGGCTGCGGAAGCTGACCCAGTGGCAGGGCTGCTGTGCCCCCTGTCATCTGAGAC 956
 CC ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 425 TGCCTTACCCATGATGCTGGTGGTGGNNNGACACCCGGCTCATGG 468
 CC ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 957 ACGCCTCACGCTGCTGATGATGGCCACACCAGCCGTGATGG 1000
 CC ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 6

ID ADR0789 standard; cDNA; 5089 BP.
 ID ADR0789; XX
 AC ADR0789; XX
 DT 04-NOV-2004 (first entry)

DE Full length human cDNA useful for treating neurological disease Seq 1395.

XX gene; BB; human; oligo-capping method; diagnostic marker; gene therapy;
 KW osteoporosis; neurological disease; Alzheimer's disease;
 KW parkinson's disease; dementia; short memory; cancer;
 KW sense or motor function; emotional reaction; fear response; panic;
 KW osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;
 KW tranquilliser.
 OS Homo sapiens.
 PN EP1447413-A2.
 XX PD 18-AUG-2004.
 XX PF 12-FEB-2004; 2004EP-00003145.
 XX PR 14-FEB-2003; 2003JP-00102207.
 PR 09-MAY-2003; 2003JP-00131457.
 PA (REAS-) RBS ASSOC BIOTECHNOLOGY.
 XX PI Isogai T, Yamamoto J, Nishikawa T, Isono Y, Sugiyama T, Otsuki T;
 PI Wakamatsu A, Ishii S, Nagai K, Irie R;
 XX WPI: 2004-583265/57.
 DR P-PSDB; ADR09845.

This invention relates to novel, isolated full length human cDNA molecules and the encoded proteins thereof. Specifically, it refers to molecules obtained by an oligo-capping method, where none of these DNA clones obtained by an oligo-capping method, where none of these clones are identical to any known human mRNAs. The present invention describes an immunassay to identify agonists and antagonists, as well as antibodies, antisense molecules and siRNAs that can all be used to bind

CC to and modulate expression of the cDNA molecules. As such, these molecules are useful for diagnostic markers or therapeutic targets for the various diseases or morbid states. In particular, they are useful in gene therapy for treating osteoporosis, neurological disease, Alzheimer's disease, Parkinson's disease, dementia, short memory and various cancers, as well as for maintaining equilibrium of sense or motor function, and for treating emotional reaction, fear response and panic. Accordingly, they exhibit osteoprotective, neuroprotective, nootropic, anti-parkinsonian, cytoactive and tranquiliser activities. This polynucleotide is a full length human cDNA sequence of the invention. NOTE: This sequence is not given in the sequence listing of the specification but can be obtained on CD-ROM from the European Patent Office, Vienna Sub-office.

XX Sequence 5089 BP; 891 A; 1705 C; 1495 G; 998 T; 0 U; 0 other;

SQ Query Match 67.5%; Score 316; DB 13; Length 5089;
 Best Local Similarity 78.9%; Pred. No. 1.3e-80;
 Matches 366; Conservative 0; Mismatches 97; Indels 1; Gaps 1;

Db QY 5 GAGTCGCTTGGTGGGGACTAGTGAATGTCAGATGCCCTGCTCTGGCCAGCTG 64
 Db QY 610 GAGCTGCGCTTGGGGGGGGACTCGTGTGATGTACAGTCCCCTGCTCTGGCCAGCTG 669
 QY 65 GTGGAGATTGGGCCAGTACAGGACACATGGGAGCTNCTGTTGANTCCCG 124
 Db 670 GTAGAGSTCGTGGCCAGTAGTACAGAAGGACCGTGTGACTGAGTCAG 729
 Db QY 125 AAGCTCANCAGNCANCTGCTCTACTGNACAGAGTCAGGAACTTGACCTTNGATAC 184
 CC ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 730 AACTCAGCACCCACCTGCTTATCCCTATCTGCTGCTGAGCACTGTGACTTCGGTAC 789
 QY 185 CTAGTCTGTGCTGCCACATGCTTATCCCTATCTGCTGCTGAGCACTGTGACTTCGGTAC 244
 CC ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 790 CTGGTGTGCTGCTGCCACGGTGGCTGGAGGCGATGGCTGTGGACATGGCGAGGSCCCCTTC 849
 QY 245 AAGCTCCCTGCTGGAGAGATTCAGGTTNTTGTAGTCCAAAGAGCAGGCGATGGTGT 304
 CC ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 850 AAGCTCCTGCTGCTGCCACGGTGGCTGGAGGCGATGGCTGTGGACATGGCGAGGSCCCCTTC 908
 QY 305 GAGTCGCTGTACTACTATGTCAGAAGATTCAGGATCTTNAAGCTGTCATINCCA 364
 CC ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 909 GAGCCGTTGACGACTAGTGGAGGTTAGTCCTCTTCACAGTCATCCCA 968
 QY 365 GAGACTGTGCACTGTGAGCTGAGCTGTTAGTGGAGGCTGAGAGCTGAGCTGAGCTG 424
 CC ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 969 GAGGCTGCGGAAGCTGACCCAGTGGCAGGGCTGCTGTGCTGCCCCCTGTCATCTGAGAC 1028
 QY 425 TGCCTTACCCATGATGCTGGTGGTGGNNNGACACCCGGCTCATGG 468
 CC ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1029 ACGCCTCACGCTGCTGATGATGGCCACACCAGCCGTGATGG 1072

RESULT 7

ID AAC76613 standard; cDNA; 1211 BP.
 ID AAC76613; XX
 AC AAC76613; XX
 DT 08-FEB-2001 (first entry)

XX DE Human ORF X ORF2168 polynucleotide sequence SEQ ID NO:4335.

XX Human; open reading frame; ORF; detection; cytostatic; hepatotropic; vulnerability; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarrhythmic; immunosuppressant; carcitant; immunomimulant; thrombotic; coagulant; vasodilator; hypotensive; dermatological; immunosuppressive; antiinflammatory; anti-viral; antibacterial; antifungal; anti-rheumatic; antithyroid; aniaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma;

KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
 KW bone damage; cartilage damage; antiinflammatory disease; coagulation;
 KW thrombosis; contraceptive; ss.
 OS Homo sapiens.
 PN WO20058473-A2.
 XX
 PD 05-OCT-2000.
 XX
 PP 31-MAR-2000; 2000WO-US008621.
 XX
 PR 31-MAR-1999; 99US-0127607P.
 PR 02-APR-1999; 99US-0127636P.
 PR 05-APR-1999; 99US-0127728P.
 PR 30-MAR-2000; 2000US-00540763.
 XX
 PA (CURA-) CIRAGEN CORP.
 XX
 PI Shimkets RA; Leach M;
 XX
 DR MPI; 2000-602362/57.
 DR P-PSDB; AAB42404.
 XX
 PT Novel nucleic acids and peptides derived from open reading frame X,
 useful for treating e.g. cancers, proliferative disorders,
 neurodegenerative disorders and cardiovascular disease.
 XX
 PS Claim 5; Page 3530-3531; 5507BP; English.
 CC AAC7446 to AAC77605 encode the proteins given in AAB40237 to AAB4337,
 which represent the human ORF X open reading frames 1 to 3161. The ORF X
 sequences have activities such as: cytotoxic; hematotropic; vulnerary;
 antiparotic; anti-parkinsonian; nootropic; neuroprotective; osteopathic;
 anticonvulsant; antiarthritic; immunosuppressant; immunostimulant;
 cardiotonic; thrombotic; coagulant; vasotropics; antidiabetic; hypotensive;
 dermatological; immunosuppressive; antiinflammatory; antibacterial;
 antiviral; antifungal; antiarthritic; antithyroid; and antianemic. The
 sequences have been used for determining the presence of or predisposition
 to, or preventing or treating pathological condition associated with an
 ORF X-associated disorder. The nucleic acids can be used to express ORF X
 proteins in gene therapy vectors. The proteins and nucleic acids may be
 used to treat cancers, proliferative disorders, neurodegenerative
 disorders, osteoarthritis, graft vs host disease, cardiovascular disease,
 diabetes mellitus, hypertension, hypothyroidism, cholesterol ester
 storage, systemic lupus erythematosus, severe combined immunodeficiency
 (SCID), AIDS, viral, bacterial or fungal infection, malaria, asthma, autoimmunity
 disorders, allergies, aplastic anaemia, burns, wounds, bone and
 cartilage damage, nocturnal hemoglobinuria, antiinflammatory disease, to
 enhance coagulation; to inhibit thrombosis; and as a contraceptive
 XX Sequence 1211 BP; 228 A; 372 C; 358 G; 253 T; 0 U; 0 Other;
 SQ

Query Match 67.3%; Score 315; DB 3; length 1211;
 Matches 365; Conservative 0; Mismatches 97; Indels 1; Gaps 1;

QY 6 AGCTGCGCTTGGTGGCGCACTAGTATGAGATGGCAGATCCCTTGCTCGCGCAGCTG 65
 Db 119 AGCTGGCTTCCTGGTGGCGCACTGGTGGATGAGATGGCAGATCCCTTGCTCGCGCAGCTG 178
 QY 66 TAGAGATGTGCCAGTACAGGAGGACCATGGGAGTNCNTGNTGANTCCGNA 125
 Db 179 TAGAGGGTGTGGCGAGTACAGGAGGACCATGGGAGTTCAGTGGAGTTCA 238
 QY 126 AGCTCANCGNCCANCTGCTCTACTGAGACAGTCAGGNAGTGTGAGCTTGGATACC 185
 Db 239 ATCTCAGCACCCACCTCTTATCTCTATGTTGCTCCAGGGACTGTCACCTTCGGTAC 298
 QY 186 TAGTAGCTGCTGTCGCCACATTGNGANCAGTCAGTGGAAAGCCCTTTCA 245
 Db 299 TGTGCTGCTGTCGCCAGTTCAGGAGGACCATGGTGGAGATGGAGGAGCCCTTC 358

RRESULT 8
 AAH18672
 ID AAH18672 standard; cDNA; 2383 BP.
 XX
 AC AAH18672;
 XX
 DT 26-JUN-2001 (first entry)
 XX Human cDNA sequence SEQ ID NO:18919.
 KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
 XX
 OS Homo sapiens.
 XX
 PR 28-JUL-2000; 20000SP-00116126.
 XX
 PR 29-JUL-1999; 99JJP-00248036.
 XX
 PR 27-AUG-1999; 99JJP-00300253.
 XX
 PR 11-JAN-2000; 20000JP-00118776.
 XX
 PR 02-MAY-2000; 20000JP-00183367.
 PR 09-JUN-2000; 20000JP-00241899.
 XX
 PR (HELI-) HELIX RES INST.
 XX
 PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 DR WPI; 2001-318749/34.

PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
 XX
 PR Claim 8; SEQ ID NO 18919; 253TP + Sequence Listing; English.
 XX
 CC The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises:
 CC (a) an oligo-dT primer and an oligonucleotide complementary to the
 CC complementary strand of a polynucleotide which comprises one of the 5602
 CC nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in the
 CC specification. The primer sets can be used in antisense therapy and in
 CC gene therapy. The primers are useful for synthesising polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 detection and/or diagnosis of the abnormality of the proteins encoded by

Best Local Similarity 80.1%; Pred. No. 2e-49; Mismatches 57; Indels 0; Gaps 0;

Matches 229; Conservative 0; N mismatches 57; Indels 0; Gaps 0;

Db 180 GCTGAGCGCGTGTGACAATGAGCTGGAGGTTAAGTCATCCTCAGCTGTCTC 239

Oy 362 CGAGGACTGCGAGCTGNNACCCAGGTGATTGGTAGCTTGCTGAGAGCTGNTATGNC 421

Db 240 CGAGGACTGCGANCTGCAACCCAGGTGCGAGCTGGCTGCTGATGTC 299

QY 422 CCCTCGGCTTAACCTGATGCTGCTGNGNCAACCCGCCCTCATGG 468

Db 300 GACACGCTCAGNCCTCTGCTGATGGGGGCCAACACAGGCCATGG 346

RESULT 13

ACH43729 ID ACH43729 standard; cDNA; 494 BP.

XX AC ACH43729;

AC Human; ss; Sequencing by hybridisation; SBH; expressed sequence tag; EST; genome mapping; biodiversity; genetic disorder.

KW genome mapping; biodiversity; genetic disorder.

XX OS Homo sapiens.

XX PN US2003073423-A1.

PD 17-APR-2003.

XX PP 30-JUL-2001; 2001US-00918995.

PR 30-JUL-2001; 2001US-00918995.

XX PA (DRMA/) DRMANAC R T.

PA (LABA/) LABAT I.

PA (STAC/) STACHE-CRAIN B.

PA (DICK/) DICKSON M C.

PA (JONE/) JONES L W.

XX PI Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW,

XX DR MPI; 2003-615964/58.

XX PT New polynucleotide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA.

XX PS Claim 1; SEQ ID NO 30941; 44pp; English.

The invention relates to an isolated polynucleotide comprising any one of 38043 cDNA sequences, appearing as ACH1289-ACH5031, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polynucleotide. The nucleic acid sequences are useful in diagnostics as expressed sequence tags (EST) for identifying expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversity, or in identifying mutations, responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA. The purified polypeptide is useful for generating antibodies specific for it. The present sequence is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DOCID=20030073623

XX SQ Sequence 494 BP; 84 A; 158 C; 135 G; 108 T; 0 U; 9 Other;

Query Match 44.2%; Score 206.8; DB 9; Length 494;

RESULT 14

AAF22411 ID AAF22411 standard; cDNA; 1023 BP.

XX AC AAF22411;

XX DT 26-MAR-2001 (first entry)

XX Human secreted protein gene 39 SEQ ID NO:49.

XX PA Human; Secreted protein; diagnosis; immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytotoxic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; ophthalmological; gene therapy; autoimmune disease; neoplasm; rheumatoid arthritis; hyperproliferative disorder; cardiac arrest; cardiovascular disorder; cerebrovascular disorder; cerebral ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; infection; ocular disorder; corneal infection; wound healing; skin ageing; food additive; preservative; ss.

XX OS Homo sapiens.

XX PN WO2000061629-A1.

PD 19-OCT-2000.

XX PP 06-APR-2000; 2000WO-US009071.

PR 09-APR-1999; 99US-012664P.

PR 20-JAN-2000; 2000US-017931P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

PA (ROSE-) ROSEN C A.

XX PI Ruben SM, Komatsoulis G;

XX DR WPI: 2000-647420/62.

DR P-PSDB; AAB63172.

PT Isolated nucleic acid molecule encoding a human secreted protein is used in preventing, treating or ameliorating a medical condition.

XX PS Claim 1; Page 450-451; 533pp; English.

XX AAF22373 to AAF22421 encode the human secreted proteins given in AABC63134 to AAB63182. AAB63183 to AAB6321 represent more human secreted proteins and polypeptides homologous to them. Human secreted proteins have activities based on the tissues and cells the genes are expressed in. Examples of activities include: immunosuppressive; antiarthritic;

CC antirheumatic; anti-proliferative; cytostatic; cardiotonic; vasotropic;
 CC cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;
 CC fungicide; and ophthalmological. The polynucleotides and proteins can be
 used to prevent, treat or ameliorate a medical condition in e.g. humans,
 mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are
 also used in diagnosing a pathological condition or susceptibility to a
 pathological condition. Disorders which are diagnosed or treated include
 autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
 disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
 e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,
 angiogenesis, nervous system disorders e.g. Alzheimer's disease,
 infections caused by bacteria, viruses and fungi and ocular disorders
 e.g. corneal infection. The polypeptides can also be used to aid wound
 healing and epithelial cell proliferation, to prevent skin aging due to
 culture of primary tissues, to regenerate tissues and in phototoxicity. The
 polypeptides can also be used as a food additive or preservative to
 increase or decrease storage capabilities. AAH22364 to AAH22772 and
 AAB63133 represent sequences used in the exemplification of the present
 invention.

PR 27-AUG-1999; 99JP-00300253.
 PR 11-JAN-2000; 2000JP-0018776.
 PR 02-MAY-2000; 2000JP-00183767.
 PR 09-JUN-2000; 2000JP-00241899.
 XX PA (HELI-) HELIX RES INST.
 XX PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 XX Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 XX DR WPI; 2001-31879/34.

XX PS Claim 1; SEQ ID NO 5246; 253pp + Sequence Listing; English.
 XX The present invention describes primer sets for synthesising 5602 full-
 length cDNAs defined in the specification. Where a primer set comprises:
 CC (a) an oligo-dt primer and an oligonucleotide complementary to the
 CC complementary strand of a polynucleotide which comprises one of the 5602
 CC nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in the
 CC specification. The primer sets can be used in antisense therapy and in
 CC gene therapy. The primers are useful for synthesising polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH0166 to AAH1362 and
 CC AAH1363 to AAH8742 represent human cDNA sequences; AAB9246 to AAB9593
 CC represent human amino acid sequences; and AAH1362 to AAH1362 represent
 CC oligonucleotides, all of which are used in the exemplification of the
 present invention.

XX SQ Sequence 744 BP; 117 A; 249 C; 205 G; 171 T; 0 U; 2 Other;
 XX Query Match 39.8%; Score 186.2.; DB 4; Length 744;
 XX Best Local Similarity 79.4%; Pred. No. 2.1e-43; 0; Mismatches 58; Indels 2; Gaps 2;
 XX Matches 231; Conservative 58; Indels 2; Gaps 2;

Db 420 GTGCTGCCTGGGTGCGGCCACTCTGTGAATGTCAGAATCCCCTGCTTGCCAGT- 478
 QY 5 GAGCTGCCTTAGGTGGCGCACTAGTAATGTCAGAATGTCAGAATCCCCTGCTTGCCAGT- 478
 Db 420 GTGCTGCCTGGGTGCGGCCACTCTGTGAATGTCAGAATCCCCTGCTTGCCAGT- 478
 QY 65 GAGCTGCCTTAGGTGGCGCACTAGTAATGTCAGAATGTCAGAATCCCCTGCTTGCCAGT- 478
 Db 479 GTAGAGGTGTCGGCAAGTACAGAACAGAGTTCAATGAGTCAGCTCCAG 538
 QY 125 AAGCTCAGCCGCACTGCTCTACTGACAGTCAAGCTGTTAGGACTGTTAGT 184
 Db 539 AACCTCTGCACTGCTCTGCAACCTTGCGGAGCAGTGTGAGCTGCTCGAGGCTCTTC 598
 QY 185 CTAGTGCTCTGTCGCACTGCTCTGCAACCTTGCGGAGCAGTGTGAGCTGCTCGAGGCTCTTC 244
 Db 599 CTGGTGCTCTGCAACCTTGCGGAGCAGTGTGAGCTGCTCGAGGCTCTTC 658
 QY 245 AGCTCCCTCTCTGCAACCTTGCGGAGCAGTGTGAGCTGCTCGAGGCTCTTC 294
 Db 659 AGCTCCCTCTCTGCAACCTTGCGGAGCAGTGTGAGCTGCTCGAGGCTCTTC 709

RESULT 15
 AAH08411 AAH08411 standard; cDNA; 744 BP.
 XX AC AAH08411;
 XX DT 26-JUN-2001 (first entry)
 XX DE Human cDNA clone (5'-primer) SEQ ID NO:5246.
 XX KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; SB.
 OS Homo sapiens.
 XX PN EP1074617-A2.
 XX PD 07-FEB-2001.
 XX PP 28-JUL-2000; 2000EP-00116126.
 XX PR 29-JUL-1999; 99JP-00248036.

Search completed: January 20, 2006, 20:40:51
 Job time : 475 secs

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Om nucleic - nucleic search, using bw model

Run on: January 20, 2006, 19:56:09 ; Search time 3081 Seconds

(without alignments)
7106.899 Million cell updates/sec

Title: US-10-327-713-267

perfect score: 468

Sequence: 1 gactgaggtggcccttaaggcg.....ngnacaccgcctatgg 468

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gabext 1.0

Searched: 41078325 seqs, 2339541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

BST:*

1: gb_est1:*

2: gb_est2:*

3: gb_est3:*

4: gb_htc:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_est7:*

9: gb_gb81:*

10: gb_gb82:*

11: gb_gb83:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

Result No.	Score	Query	Match Length	DB	ID	Description
1	436	93.2	468	10	CG663507	CG663507 OS448795
2	415	88.7	751	6	CB249142	CB249142 UI-MFC0-
3	415	88.7	1659	4	AK01688	AK01688 Mus musculus
4	415	88.7	2154	10	AY407420	AY407420 Mus musculus
5	415	88.7	2647	4	AK049152	AK049152 Mus musculus
6	415	88.7	2669	4	AK038760	AK038760 Mus musculus
7	415	88.7	2676	4	AK014319	AK014319 Mus musculus
8	415	88.7	2779	4	AK030524	AK030524 Mus musculus
9	414	88.5	780	6	CA945430	CA945430 UI-MFD0-
10	411.8	88.0	2699	6	AK076315	AK076315 Mus musculus
11	400.2	85.5	553	8	CX211935	CX211935 MNS1502
12	392.8	83.9	771	2	BI147958	BI147958 602912678
13	329.2	70.3	6	CF726195	CF726195 UI-M-G20-	
14	321.2	68.6	3	BI738314	BI738314 603361553	
15	317.6	67.9	4340	4	CR857093	CR857093 Pongo pygmaeus
16	316	67.5	2672	3	BM78757	BM78757 UI-B-EJ1-
17	316	67.5	625	3	BM783111	BM783111 K-EST0060
18	316	67.5	674	3	BM930206	BM930206 UI-B-EJ1-
19	316	67.5	1484	4	CR59833	CR59833 full-length
20	316	67.5	1553	4	CR610778	CR610778 full-length
21	316	67.5	1553	4	CR616094	CR616094 full-length
22	316	67.5	1594	4	CR592221	CR592221 full-length

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

BST:*

1: gb_est1:*

2: gb_est2:*

3: gb_est3:*

4: gb_htc:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_est7:*

9: gb_gb81:*

10: gb_gb82:*

11: gb_gb83:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

Result No.	Score	Query	Match Length	DB	ID	Description
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3	415	88.7	1659	4	AK01688	AK01688 Mus musculus
4	415	88.7	2154	10	AY407420	AY407420 Mus musculus
5	415	88.7	2647	4	AK049152	AK049152 Mus musculus
6	415	88.7	2669	4	AK038760	AK038760 Mus musculus
7	415	88.7	2676	4	AK014319	AK014319 Mus musculus
8	415	88.7	2779	4	AK030524	AK030524 Mus musculus
9	414	88.5	780	6	CA945430	CA945430 UI-MFD0-
10	411.8	88.0	2699	6	AK076315	AK076315 Mus musculus
11	400.2	85.5	553	8	CX211935	CX211935 MNS1502
12	392.8	83.9	771	2	BI147958	BI147958 602912678
13	329.2	70.3	6	CF726195	CF726195 UI-M-G20-	
14	321.2	68.6	3	BI738314	BI738314 603361553	
15	317.6	67.9	4340	4	CR857093	CR857093 Pongo pygmaeus
16	316	67.5	2672	3	BM78757	BM78757 UI-B-EJ1-
17	316	67.5	625	3	BM783111	BM783111 K-EST0060
18	316	67.5	674	3	BM930206	BM930206 UI-B-EJ1-
19	316	67.5	1484	4	CR59833	CR59833 full-length
20	316	67.5	1553	4	CR610778	CR610778 full-length
21	316	67.5	1553	4	CR616094	CR616094 full-length
22	316	67.5	1594	4	CR592221	CR592221 full-length

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

BST:*

1: gb_est1:*

2: gb_est2:*

3: gb_est3:*

4: gb_htc:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_est7:*

9: gb_gb81:*

10: gb_gb82:*

11: gb_gb83:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

Result No.	Score	Query	Match Length	DB	ID	Description
1	436	93.2	468	10	CG663507	CG663507 OS448795
2	415	88.7	751	6	CB249142	CB249142 UI-MFC0-
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5	415	88.7	2647	4	AK049152	AK049152 Mus musculus
6	415	88.7	2669	4	AK038760	AK038760 Mus musculus
7	415	88.7	2676	4	AK014319	AK014319 Mus musculus
8	415	88.7	2779	4	AK030524	AK030524 Mus musculus
9	414	88.5	780	6	CA945430	CA945430 UI-MFD0-
10	411.8	88.0	2699	6	AK076315	AK076315 Mus musculus
11	400.2	85.5	553	8	CX211935	CX211935 MNS1502
12	392.8	83.9	771	2	BI147958	BI147958 602912678
13	329.2	70.3	6	CF726195	CF726195 UI-M-G20-	
14	321.2	68.6	3	BI738314	BI738314 603361553	
15	317.6	67.9	4340	4	CR857093	CR857093 Pongo pygmaeus
16	316	67.5	2672	3	BM78757	BM78757 UI-B-EJ1-
17	316	67.5	625	3	BM783111	BM783111 K-EST0060
18	316	67.5	674	3	BM930206	BM930206 UI-B-EJ1-
19	316	67.5	1484	4	CR59833	CR59833 full-length
20	316	67.5	1553	4	CR610778	CR610778 full-length
21	316	67.5	1553	4	CR616094	CR616094 full-length
22	316	67.5	1594	4	CR592221	CR592221 full-length

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

BST:*

1: gb_est1:*

2: gb_est2:*

3: gb_est3:*

4: gb_htc:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_est7:*

9: gb_gb81:*

10: gb_gb82:*

11: gb_gb83:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

Result No.	Score	Query	Match Length	DB	ID	Description
1	436	93.2	468	10	CG663507	CG663507 OS448795
2	415	88.7	751	6	CB249142	CB249142 UI-MFC0-
3	415	88.7	1659	4	AK01688	AK01688 Mus musculus
4	415	88.7	2154	10	AY407420	AY407420 Mus musculus
5	415	88.7	2647	4	AK049152	AK049152 Mus musculus
6	415	88.7	2669	4	AK038760	AK038760 Mus musculus
7	415	88.7	2676	4	AK014319	AK014319 Mus musculus
8	415	88.7	2779	4	AK030524	AK030524 Mus musculus
9	414	88.5	780	6	CA945430	CA945430 UI-MFD0-
10	411.8	88.0	2699	6	AK076315	AK076315 Mus musculus
11	400.2	85.5	553	8	CX211935	CX211935 MNS1502
12	392.8	83.9	771	2	BI147958	BI147958 602912678
13	329.2	70.3	6	CF726195	CF726195 UI-M-G20-	
14	321.2	68.6	3	BI738314	BI738314 603361553	
15	317.6	67.9	4340	4	CR857093	CR857093 Pongo pygmaeus
16	316	67.5	2672	3	BM78757	BM78757 UI-B-EJ1-
17	316	67.5	625	3	BM783111	BM783111 K-EST0060
18	316	67.5	674	3	BM930206	BM930206 UI-B-EJ1-
19	316	67.5	1484	4	CR59833	CR59833 full-length
20	316	67.5	1553	4	CR610778	CR610778 full-length
21	316	67.5	1553	4	CR616094	CR616094 full-length
22	316	67.5	1594	4	CR592221	CR592221 full-length

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

REFERENCE	source
1. High-efficiency full-length cDNA cloning JOURNAL Meth. Enzymol. 303, 19-44 (1999)	/organism="Mus musculus" 'mol_type="mRNA" 'strain="C57BL/6J" 'db_xref="PANTOM DB:4833412N02" 'db_xref="taxon:70090" 'clone_id="4833412N02" 'tissue_type="head" 'clone_Tax="Riken full-length enriched mouse cDNA library" 'dev_stage="0 day neonate"
2 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes JOURNAL Genome Res. 10 (10), 1617-1630 (2000)	/note="AIP-binding cassette, sub-family B (MDR/TAP), member 8 (MGD:MGI:1351667, GB AF213391, evidence: BLASTN, 99%, match=370)"
3 Riken integrated sequence analysis (RISA) system--384-format Bequencing pipeline with 3'84 multicapillary sequencer JOURNAL Genome Res. 10 (11), 1757-1771 (2000)	/note="AIP-binding cassette, sub-family B (MDR/TAP), member 8 (MGD:MGI:1351667, GB AF213391, evidence: BLASTN, 99%, match=370)"
4 The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium. Functional annotation of a full-length mouse cDNA collection JOURNAL Nature 409, 685-690 (2001)	Query Match 88.7%; Score 415; DB 4; Length 1659; Best Local Similarity 91.9%; Pred. No. 2. 8e-107; Matches 429; Conservative 0; Mismatches 37; Indels 1; Gaps 1;
5 The RIKEN Consortium and the RIKEN Genome Exploration Research REFERENCE Team The PANTOM Consortium and the RIKEN Genome Exploration Research AUTHORS Group Phase I & II Team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs JOURNAL Nature 420, 563-573 (2002)	Qy 2 ACTGAGGTGGCTTAGGGCGACTAGTGATGCCAGATCCCTGCTGCACAG 61 Db 493 ATGGCTCTGGCTTGTGCGCACTAGTGATGATGTCAGATGCCCTTGCTCTGGACAG 552
6 (bases 1 to 1659) Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K., Hirao,T., Horii,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T., Kato,H., Kawai,J., Koima,Y., Konno,H., Kouda,M., Koya,S., Kuribara,C., Matsumoto,T., Miyazaki,A., Nishi,H., Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okida,T., Owa,C., Saito,H., Saito,R., Sakai,C., Sakai,H., Sano,H., Sasaki,D., Shibaoka,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y. DIRECT Submission JOURNAL Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@bc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, fax: 81-45-503-9316)	Qy 62 CTGGTGGAGATGTCGCGAACAGACAGGGACCATGGGGAGGNTGNNTGANTCC 121 Db 553 CTGGTGGAGATGTCGCGAACAGACAGGGACCATGGGGAGGTTGCTGAGTCC 612
P <small>LEASE</small> visit our web site (http://genome.gsc.riken.jp/) for further details.	Qy 122 CENAACTCANCNCNNCTGCTCTACTGATGAGTGGAGTGTGAGCTTGGGA 181 Db 613 CGTAAGCTCAGCTCCGCTGCTCTACTGATGAGTGTGAGCTTGGGA 672
C <small>DNA</small> library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to preparation of mouse tissues. First strand cDNA was primed with a primer prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer 15' GAGAGAGAGGAGTCAGGCTTGTGTTTTTGTGTT 3', cDNA was selected before cloning. Vector: a modified pBluescript KS(+) after bulk excision from Lambda PUC I Cloning sites, 5' end: SalI; 3' end: BamHI. Host: DH5B. Location/Qualifiers	Qy 182 TACCTAGTGCTGTCGACATTTGNGANGACATGCCATGACATGCGAAGCTT 241 Db 673 TACCTAGTGCTGTCGACATTTGNGANGACATGCCATGACATGCGAAGCTT 732
COMMENT	Qy 242 TTGAGCTCCCTGCTCCGCAAGCAATTGCTTNTTGTGCCAAAGACACGGCACCGT 301 Db 733 TTGAGCTCCCTGCTCCGCAAGCAATTGCTTNTTGTGCCAAAGACACGGCACG-T 791
R <small>EPORT</small> 4	Qy 302 AGTGAGTGTGCTGACTCTGATGTCAGAAGAATCAGGCACTCTTNAAGCTGTGTCATNTN 361 Db 792 AGTGAGTGTGCTGACTCTGATGTCAGAAGAATCAGGCACTCTTCACTC 851
RESULT 4	Qy 362 CCTGGGACTGNGCAGCTGACCCAGGATGGATGTTGCTGAGNCCTGTTAGTGTGNC 421 Db 852 CCTGGGACTGNGCAGCTGACCCAGGATGGATGTTGCTGAGNCCTGTTAGTGTGNC 911
AY07420	AY07420 422 CCTCTCGCTTACCTGTGCTGCTGAGNGCAACCGCCCTCATGG 468
LOCUS	Mus musculus ABCB8 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
DEFINITION	
VERSION	AY07420.1
ACCESSION	AY07420.1 GI:3976391
SOURCE	Mus musculus (house mouse)
ORGANISM	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciuromorphi; Muroidea; Muridae; Murinae; Mus
REFERENCE	1 (bases 1 to 2154)
AUTHORS	Clark,A.G., Glanowski,S., Nelson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Cavello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
FEATURES	

JOURNAL	Science 302 (5652), 1960-1963 (2003)
PUBLISHED	14571302
REFERENCE	2 (bases 1 to 2154)
AUTHORS	Clark,A.G., Gianiowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tenenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreria,S., Wang,G., Zheng,X.H., White,T.J., Sainsky,J.J., Adams,M.D. and Cagill,M.
TITLE	Direct Submission
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.
FEATURES	Location/Qualifiers
source	1. 2154 /organism="Mus musculus" /mol_type="Genomic DNA" /db_xref="taxon:10090" <1..>2154 'gene="ASCBB8" '/locus_tag="HCM2884"
ORIGIN	
Query Match	Best Local Similarity 98.7%; Score 415; DB 10; Length 2154;
Matches	429; Conservative 0; Mismatches 37; Indels 1; Gaps 1;
QY	2 ACTGACGTGGCTTATGGTGCGCACTAGTGATGTCAGATCCCTTGCTCTGGCCAG 61
Db	400 ATTTGCTGCGCTTAGGTGCGGACTAGTGATGTCAGATCCCTTGCTCTGGCCAG 459
QY	62 CTGGTGGAGATGTCGCCAACATACAGGGACACATGGGAGGAGTNCNTGANTCC 121
Db	460 CTGGTGGAGATGTCGCCAACATACAGGGACACATGGGAGGAGTNCNTGANTCC 519
QY	122 CGAAGCTCAGNCANCCTGCTCTACTGAGAAGCTGGAGACTGTCAGCTTGA 181
Db	520 CTAAGTCAGGTCAGCTTCTACTGTAGGGTTCGGAGCTGTCACCTTGA 579
QY	182 TACCTAGTGTCTGTGCCACATTGNGANCATGCCATGCGAAAAGCCCTT 241
Db	580 TACCTAGTGTCTGTGCCACATTGTTGAGGCATGCCATGGACATGCGAAAGCCCTT 639
QY	242 TTCAAGTCCTCTCGCGAACAGATGCTTNTTGTGCAAAAGACGGGAGCT 301
Db	640 TTCAAGTCCTCTCGCGAACAGATGCTTNTTGTGCAAAAGACGGGAGCT 698
QY	302 AATGAGTGTGACTRACTGTGTCAGAATTCAAGGATCTTNAAGCTGTGCAINTN 361
Db	699 AGTGAAGTGTGACTACTGTGTCAGAATTCAAGTGTGCACTTC 758
QY	362 CCAGGGACTGNCAGCTGNAACCCAGGGATTGTTGAGCTGGAGNCCTGNNATATGCTGNC 421
Db	759 CGAGGACTGGCAGCTGCAACCAGGGATTGTTGAGCTGGTGCCTGTCATGTC 818
QY	422 CCCTCGCTTACCTGATGCTGGCTGTCAGGACACCCGCCCCATCG 468
Db	819 CCCTCGCTTACCTGATGCTGGCTGTCAGGACACCCGCCCCATCG 865
RESULT	5
AK049152	AK049152 2647 bp mRNA linear HTC 03-APR-2004
LOCUS	Mus musculus ES cells cDNA, RIKEN full-length enriched library, clone:C330007P20 product:ATP-binding cassette, sub-family B (MDR/TAP), member 8, full insert sequence.
DEFINITION	(MDR/TAP), member 8, full insert sequence.
ACCESSION	AK049152
VERSION	AK049152.1
KEYWORDS	HTC; CAP trapper. Mus musculus (house mouse)
ORGANISM	Buhyo, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Eutheriontognates; Gliridae; Rodentia; Scurognathidae; Muridae; Murinae; Mus.
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CDS
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85 .2238
/note="unnamed protein product: ATP-binding cassette,
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GB|AF213391, evidence: BLASTN, 99%, match=370)
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YTRDNGSFVSERSKISVOLLINLYGVGLLUPGYVYLISHGERMAMDRMWERKAFLSLLR
RQDIAFDKKTGQLISRLTVQEPKSFKEVLSQGURSTQVLSVLMSLSPRL
TMLAVVTPALMGVTGMSGKURKURSQCORIARANGVADALGNVRTRAFAEMKR
ERRYORKELESCCKBRLGNGLQSLNATCMLVSLPFGSVLQGOKLGGD
LMSFLVJASQTQRMASLUSVIFGQVRLGSLGARVFEYMAISPVLTGCVIPKDI
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ORIGIN

Query Match 88.7%; Score 415; DB 4; Length 2647;
Best Local Similarity 91.9%; Pred. No. 3.1e-107; Mismatches 37; Indels 1; Gaps 1;
Matches 429; Conservative 0; Mismatches 37; Indels 1; Gaps 1;

QY	2	ACTAGAGCTGCCCTTAGGTTGGGACTAGTGAAATGTCAGAGCCCTTGCTGGCGAG	61
Db	484	ATTTGGCTGAGATTGGCCAGATAACGGAGCACATGGGAGTNCAGTGTGANTCC	543
QY	62	CTGGCTGGAGATTGGCCAGATAACGGAGCACATGGGAGTNCAGTGTGANTCC	121
Db	544	CTGGCTGGAGATTGGCCAGATAACGGAGCACATGGGAGTNCAGTGTGAGTC	603
QY	122	CGNAAGCTCANCNCANCCTGCTCTACTGNAACNGAGTTCAAGENACTTGCTTNGA	181
Db	604	CGTAAGCTCAGCAGTCAGCTCTACTGTTACGGACTGCTGACCTTGA	663
QY	182	TACCTAGTGTGTCTCCCATTTGNGANONCATGGCCATGNAACATGGGAAGCCTT	241
Db	664	TACCTAGTGTGTCTCCCATTTGNGANONCATGGCCATGNAACATGGGAAGCCTT	723
QY	242	TTCACTCTCTGCTCGGAGAACATGGCTTNTTGATGCCAAAGAACAGGAGCAGCT	301
Db	724	TTCACTCTCTGCTCGGAGAACATGGCTTNTTGATGCCAAAGAACAGGAGCAGCT	782
QY	302	AGTGAATCTGACTACTATGTCAGATTCAAGCTTCCTTNAAGCTTGTCATNN	361
Db	783	AGTGAATCTGACTACTATGTCAGATTCAAGTTCAAGTCACTTCCTTCAGCTTC	842
QY	362	CCAGGAGACTGCACTGNAACCCAGGTATGGTGGAGCTGAGAGCCCTGTTCTGC	421
Db	843	CCAGGAGACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCA	902
QY	422	CCCTGCCTTACCCCTGATGCTGGCTGGGAGCTGAGCTGCTGCTGCTGCTGCTG	468
Db	903	CCCTGCCTTACCCCTGATGCTGGCTGGGAGCTGAGCTGCTGCTGCTGCTGCTG	949

RESULT 6

AK038760 AK038760 2669 bp mRNA linear HTC 03-APR-2004
LOCUS DEFINITION Mus musculus adult male hypothalamus cDNA, RIKEN full-length enriched library, clone:A230060K10 product:ATP-binding cassette, sub-family B (MDR/TAP), member 8, full insert sequence.

ACCESSION AK038760
VERSION 1
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE Carninci, P. and Hayashizaki, Y.
AUTHORS Carninci, P. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
PUBMED 10349636
2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Kita, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, Y., Yamamoto, R., Matsunoto, H., Sakaguchi, S., Inagami, T., Kashiwagi, K., Fujikawa, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanuki, M., Yoneda, Y., Ishikawa, T., Ozawa, Y., Matsunura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384-microcapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
4 11076861

JOURNAL The RIKEN Genome Exploration Research Group Phase II Team and the
PANTOM Consortium
REFERENCE Carninci, P., Akiyama, J., Nishi, K., Kita, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, Y., Yamamoto, R., Matsunoto, H., Sakaguchi, S., Inagami, T., Kashiwagi, K., Fujikawa, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanuki, M., Yoneda, Y., Ishikawa, T., Ozawa, Y., Matsunura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
5 The PANTOM Consortium and the RIKEN Genome Exploration Research
AUTHORS Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
6 (bases 1 to 2669)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, M., Hayashida, K., Hayatsu, N., Hisamoto, K., Hirakawa, T., Hirozane, T., Horii, F., Imotani, I., Ishii, Y., Kondo, S., Kono, H., Kouda, M., Katoh, H., Kawai, J., Kojima, Y., Konod, S., Murata, M., Nagayama, T., Miyazaki, A., Murata, M., Ohbayo, N., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ono, M., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku, Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toyai, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
TITLE Direct Submission
JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-research.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: +81-45-503-9222, Fax: +81-45-503-9216)

COMMENT cdNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details.
FEATURES URL: http://fantron.gsc.riken.jp/
source Location/Qualifiers
1 . 2659
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/strain="C57BL/6J"
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VERSION	AK030624.1
KEYWORDS	CAP trapper; HTC; CAP trapper;
ORGANISM	Mus musculus
REFERENCE	Mammalia; Buterida; Euarctontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buterida; Euarctontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
JOURNAL	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buterida; Euarctontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	Carninci, P., and Hayashizaki, Y.
AUTHORS	Carninci, P., and Hayashizaki, Y.
JOURNAL	High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999)
REFERENCE	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Otaasaki, Y., Muramatsu, M., and Hayashizaki, Y.
AUTHORS	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
JOURNAL	Shibata, K., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kasahagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, B., Watariki, M., Oneda, Y., Ishikawa, T., Ozawa, S., Matsubara, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.
REFERENCE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
AUTHORS	11076861
JOURNAL	PUBMED
REFERENCE	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium. Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
AUTHORS	Group Phase I & II Team.
JOURNAL	5
REFERENCE	The RIKEN Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002)
AUTHORS	(bases 1 to 2779)
JOURNAL	6
REFERENCE	Adachi, J., Araiwa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, M., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirakawa, T., Hirozawa, T., Horii, P., Imori, K., Ishii, Y., Itoh, M., Kagawa, I., Sano, H., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Ohshato, N., Ozaaki, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, P., Tokuno-Akaihira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.
AUTHORS	Direct Submission
JOURNAL	Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-reseqbc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: +81-45-503-9222, Fax: +81-45-503-9216).
COMMENT	cdna library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken

RESULT 9

CAB45430

LOCUS CA945430

DEFINITION U1-M-FD0-cdh-p-24-0-U1.r1 NIH BNAP_FDO Mus musculus cDNA clone

ACCESSION CA945430

VERSION CA945430.1

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

COMMENT Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Branchiotolires; Glires; Rodentia; Sciuromorpha; Muridae; Murida; Murinae; Mus.

REFERENCE 1 (bases 1 to 780)

AUTHORS NIH-MGC <http://mgc.ncbi.nih.gov/>

TITLE National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

CONTACT Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov

Tissue Procurement: Dr. James Lin, University of Iowa
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution by: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: <http://image.lnl.gov>

This clone was contributed by the Brain Molecular Anatomy Project (BMAP).

SEQ PRIMER: PYX-5

Location/Qualifiers

1. . 780

FEATURES

Source

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6"

/clone="IMGR:6829033"

/tissue_type="whole brain"

/dev_stage="embryo 12.5 dpc"

/lab_host="DH10B (T1 phage resistant)"

/clone_lib="NIH BNAP_FDO"

/note="Organ: brain; Vector: PYX-ASC; Site 1: EcoR I; Site 2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured DNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into PYX-ASC vector. The library tag sequence located between the Not I site and the polyA tail, is TtagAGAGCC. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP); 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institutes of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN

Query Match 88.7%; Score 415; DB 4; Length 279;

Best Local Similarity 91.9%; Pred. No. 3. 2e-107;

Matches 429; **Conservative** 0; **Mismatches** 37; **Indels** 1; **Gaps** 1;

Query 2 ACTGAGACTGGCTTAGGTGCGAGATCAAGCATCTTAAAGCTTGATNTN

Db 467 ATTTGTGTGGCTTAGGTGCGAGCTAGTGATGTGGAGATCCCTTGCTGGCCAG 61

Query 62 CTTGGTGGAGATGTCGCCAGTACAGGACCATAGTGATGTGGAGATCCCTTGCTGGCCAG 61

Db 587 CTAACTGTCAGGTCAGCTGCTCTACTGTAGGGTTGCGAGCTGCTGACCTTGA 646

Query 182 TACCTAATGCTCTGTGCCAACATGGNNANGANCATGCCATGACGAAAGCCCT 241

Db 527 CTGGTGGAGATGTCGCCAACATGGACCATGGAGGACCATGGAGATTCAGTCTGAGTCC 586

Query 122 CGAAAGCTCAGGNCCANCCTGCTCTACTGAGACAGAGCTGAGCTCTGTTGGA 181

Db 587 CTAACTGTCAGGTCAGCTGCTCTACTGTAGGGTTGCGAGCTGCTGACCTTGA 646

Query 647 TACCTAATGCTCTGTGCCAACATGGAGGACATGGACCATGGAGATTCAGTCTGAGCTT 706

Db 242 TTCAAGTCCCTCTCCGGCAAGACATGTTTGTGAGGCAAAAGACGGGGGGCT 301

Query 707 TTCAAGTCCCTCTCCGGCAAGACATGTTTGTGAGGCAAAAGACGGGGGGCT 765

Db 302 ACTGAGACTGGCTTAGGTGCGAGCTAGTGATGTGGAGATCCCTTGCTCTGGCCAG 361

Query 766 ATTTGTGTGGCTTAGGTGCGAGATCAAGCATCTTAAAGCTTGATNTN

Db 825 362 CGAGGACTGNGCAGTGNACACCGAGGTGGATGTGGAGCTGCTGGCCAG 421

Db 826 CGAGGACTGCGCAGCTGCAACCGAGGTGGATGTGGAGCTGCTGGCCAG 483

Query 422 CCTCGCTTACCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGTC 468

Db 886 CCCTGCACTTACCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGTC 932

ORIGIN

Query Match 88.5%; Score 414; DB 6; Length 780;

Best Local Similarity 91.6%; Pred. No. 4.5e-107;

Matches 428; **Conservative** 0; **Mismatches** 38; **Indels** 1; **Gaps** 1;

Query 2 ACTGAGACTGGCTTAGGTGCGAGCTAGTGATGTGGAGATCCCTTGCTCTGGCCAG 61

Db 180 ATTTGTGTGGCTTAGGTGCGAGCTAGTGATGTGGAGATCCCTTGCTCTGGCCAG 239

Query 62 CTGGTGGAGATGTCGCCAGTACAGGACCATGGAGATTCAGTCTGAGCTGCTGAGTCC 121

Db 240 CTGGTGGAGATGTCGCCAGTACAGGACCATGGAGATTCAGTCTGAGCTGCTGAGTCC 299

Query 122 CGAAAGCTCAGGNCCANCCTGCTCTACTGAGACAGAGCTGAGCTCTGAGTCC 181

Db 300 CGTAAGCTCAGGTCGCCCTACTGCTACCGGGCTGACCTTGA 359

Qy	182	TACCTAGTCGCTGCTGCCACATGGANGANCAGTGCGGAAAGCCCT	241	Fukuda,S., Furuno,M., Hanagaki,T., Hara,H., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hirao,T., Hirokane,T., Horii,P., Imottani,K., Iishi,Y., Ittoh,M., Kaga,I., Kasukawa,T., Kohno,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koyai,S., Kurinara,C., Murayama,M.-T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,K., Sakazume,N., Sanoh,R., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tadawa,A., Takahashi,F., Takuji-Alahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M., and Hayashizaki,Y.		
Qy	360	TACCTAGTCGCTGCTGCCACATGGANGANCAGTGCGGAAAGCCCT	419	Hori,I., Imottani,K., Iishi,Y., Ittoh,M., Kaga,I., Kasukawa,T., Kohno,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koyai,S., Kurinara,C., Murayama,M.-T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,K., Sakazume,N., Sanoh,R., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tadawa,A., Takahashi,F., Takuji-Alahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M., and Hayashizaki,Y.		
Db	242	TTCGCTCCCTGCCCGCAAGACATTGCTTNTTGATGCCAAAAGACAGGGAGGT	301	420	TTCGCTCCCTGCCCGCAAGACATTGCTTNTTGATGCCAAAAGACAGGGAGGT	478
Qy	302	AGTGGTGCCTGAATCTGATGTCAGAAGATCAGGACCTTNAAGCTGCAATNN	361	AGTGGTGCCTGAATCTGATGTCAGAAGATCAGGACCTTNAAGCTGCAATNN	478	
Qy	479	AGTGGTGCCTGAATCTGATGTCAGAAGATCAGGACCTTNAAGCTGCAATNN	538	AGTGGTGCCTGAATCTGATGTCAGAAGATCAGGACCTTNAAGCTGCAATNN	538	
Db	362	CCAGGACTGCACTGAGTGNACCCAGGTGTTGGCCGAGNCCTNTATCTGC	421	362	CCAGGACTGCACTGAGTGNACCCAGGTGTTGGCCGAGNCCTNTATCTGC	421
Db	539	CCAGGACTGCACTGACCCAGGTGATGGGAGCCCTGTCCTGCTCTATCTGC	598	539	CCAGGACTGCACTGACCCAGGTGATGGGAGCCCTGTCCTGCTCTATCTGC	598
Qy	422	CCCTGGCTTACCTGATGCTGGCTGNGNACACCCGCCTCATGG	468	422	CCCTGGCTTACCTGATGCTGGCTGNGNACACCCGCCTCATGG	468
Db	599	NCCTGGCTTACCCGGATGCTGGCTGACACCCGCCTCATGG	645	599	NCCTGGCTTACCCGGATGCTGGCTGACACCCGCCTCATGG	645
RESULT 10						
DEFINITION	AK076315	Mus musculus 10 days neonate skin cDNA, RIKEN full-length enriched library, clone:4732414M12 product:ATP-binding cassette, sub-family B (MDR/TAP), member 8, full insert Sequence.	AK076315	Mus musculus 10 days neonate skin cDNA, RIKEN full-length enriched library, clone:4732414M12 product:ATP-binding cassette, sub-family B (MDR/TAP), member 8, full insert Sequence.		
ACCESSION	AK076315		AK076315			
VERSION	AK076315.1	GI:23345291	AK076315.1	GI:23345291		
SOURCE	Mus musculus (house mouse)		Mus musculus (house mouse)			
ORGANISM	Rat		Rat			
KEYWORDS	HTC; CAP trapper;		HTC; CAP trapper;			
REFERENCE	1	Carninci,P. and Hayashizaki,Y. Mus musculus; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Eukaryota; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	1	Carninci,P. and Hayashizaki,Y. Mus musculus (house mouse) High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999)		
AUTHORS						
TITLE						
JOURNAL						
PUBLMED	10349636					
REFERENCE	2	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., shibata,K., Ichijo,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)	2	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., shibata,K., Ichijo,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)		
AUTHORS						
TITLE						
JOURNAL						
PUBLMED	11042159					
REFERENCE	3	Shibata,K., Ichijo,M., Aizawa,K., Nagao,K., Saeki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitasuna,T., Tashiro,O.H., Ichijo,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishimine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kasaiwagi,K., Fujikawa,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,B., Watanuki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsubara,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)	3	Shibata,K., Ichijo,M., Aizawa,K., Nagao,K., Saeki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitasuna,T., Tashiro,O.H., Ichijo,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishimine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kasaiwagi,K., Fujikawa,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,B., Watanuki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsubara,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)		
AUTHORS						
REFERENCE	4	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium. Functional annotation of a full-length mouse cDNA collection	4	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium. Functional annotation of a full-length mouse cDNA collection		
AUTHORS						
REFERENCE	5	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs	5	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs		
AUTHORS						
REFERENCE	6	(bases 1 to 2699)	6	(bases 1 to 2699)		
AUTHORS						
REFERENCE	7	Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,	7	Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,		
ORIGIN						
Qy	2	ACTGAGCTGGCTTAGTGCGGCACTAGTGATGTCGAGACCCCTCTGGCCAG	61	Query Match Best Local Similarity 88.0%; Score 411.8; DB 4; Length 2699; Matches 427; Conservative 0; Mismatches 39; Indels 1; Gaps 1; /note="putative"		
Db	491	ATGTGCTGGCTTAGTGCGGCACTAGTGATGTCGAGACCCCTCTGGCCAG	550	2 ACTGAGCTGGCTTAGTGCGGCACTAGTGATGTCGAGACCCCTCTGGCCAG		

		Best Local Similarity	92.0%	Pred.	No.	3.6e-103;					
		Matches	413;	Conservative	0;	Mismatches	35;	Indels	1;	Gaps	1;
QY	62	CTGGTGGAGATGTCGCCAACAGTACACAGGAGCACATGGAGAGNTNCNTGANTCC	121								
Db	551	CCTGGTGGAGATGTCGCCAACAGTACACAGGAGCACATGGAGAGNTTCGTC	610								
QY	122	CNAAGCTCAGCGNCNACTCTCTTACTGTAACAGGAGCAATGCGAGTTGCG	181								
Db	611	CATAAGTCAGCTGGTCCAGCTCTACTGTAACAGGAGCAATGCGAGTTGCG	670								
QY	182	TACCTAGTGCTGTGCCAACATTGNGANCGCATGCCATGCGAAACCCCT	241								
Db	671	TACCTAGTGCTGTGCCAACATTGNGAGGCGATGCCATGCGAAACCCCT	730								
QY	242	TTCAGTCCTCTCCCGAACAGATGCTTNTGATGCCAAMAGACGGGAGGT	301								
Db	731	TTCAGTCCTCTCCCGAACAGATGCTTNTGATGCCAAMAGACGGGAGGT	789								
QY	302	AATGAGTGTGCTGACTACTGATGATGCGAGAAATCAAGGATCCTNAAGT	361								
Db	790	AATGAGTGTGCTGACTACTGATGATGCGAGAAATCAAGGATCCTNAAGT	849								
QY	362	CCAGGACTGAGCAGTGNACCGAGGATGTTGATCTGTCAGGAGTCG	421								
Db	850	CCAGGACTGAGCAGTGNACCGAGGATGTTGATCTGTCAGGAGTCG	909								
QY	422	CCCTGCCTTACCTGATGCTGCTGCTGACACCGCCCTACGG	468								
Db	910	CCCTGCCTTACCTGATGCTGCTGCTGACACCGCCCTACGG	956								
RESULT 11											
LOCUS	CX211935	553 bp mRNA	linear EST	29-DEC-2004							
DEFINITION	MN316502	Mouse Neurosphere Normalized cDNA library	Mus musculus								
ACCESSION	CX211935	CDNA 5'	mRNA sequence.								
VERSION	CX211935.1	63:5687227									
KEYWORDS	BST.										
SOURCE	Mus musculus	(house mouse)									
ORGANISM	Mus musculus										
REFERENCE	Bukay-Yosef, Metzger, Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Eutherionglires; Glires; Rodentia;										
AUTHORS	Williams, C., Wirta, V., Lundeberg, J. and Frisen, J.										
TITLE	Expressed sequence tags of cDNA clones from murine neurospheres										
JOURNAL	Unpublished (2005)										
COMMENT	Contact: Williams, C.										
RESULT 12											
LOCUS	BT147958	771 bp mRNA	linear EST	05-JUL-2001							
DEFINITION	602912678P1 NCI_CGAP_L19 Mus musculus cDNA clone										
	IMGR:5053602 5'	mRNA sequence.									
ACCESSION	BT147958										
VERSION	BT147958.1	GI:14607959									
KEYWORDS	EST.										
SOURCE	Mus musculus										
ORGANISM	Mus musculus	(house mouse)									
REFERENCE	Bukay-Yosef, Metzger, Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Eutherionglires; Glires; Rodentia;										
AUTHORS	Sciuromathi, Muroidea; Muridae; Murinae; Mus.										
TITLE	Unpublished (1999)										
JOURNAL	Contact: Robert Strauberg, Ph.D.										
COMMENT	Email: cgs@rsrmail.nih.gov										
RESULT 13											
FEATURES	Tissue Procurement:	Jeffrey B. Green, M.D.									
source	cDNA Library Preparation:	Life Technologies, Inc.									
/organism="Mus musculus"	cDNA Library Arrayed by:	The I.M.A.G.E. Consortium (LNU)									
/mol_type="mRNA"	DNA Sequencing by:	Incyte Genomics, Inc.									
/strain="CS7BL/6"	Clone distribution:	MGC clone distribution information can be									
/db_xref="taxon:10090"	found through the I.M.A.G.E. Consortium/LNU at:										
/sex="MALE"	http://image.llnl.gov										
/tissue_type="lateral wall of lateral ventricle"	Plate:	LIML1145 row: 1 column: 19									
/cell_type="Early passage neurosphere"	High quality sequence stop:	738.									
/dev_stage="Adult"	Location/Qualifiers										
/clone_lib="Mouse Neurosphere Normalized cDNA library"	1. .771										
/note="Organ: Adult brain; Vector: pcMVspor6.0; A cDNA library was constructed in pcMVspor6.0 from RNA isolated from neurospheres of adult male and female mice. Custom normalized cDNA library by Invitrogen/ResGen"	/organism="Mus musculus"										
ORIGIN	/mol_type="mRNA"										
	/strains="PVB/N"										
	/db_xref="taxon:10090"										
	/clone="IMAGE:5055602"										
	/lab_host="DH10B (T1 phage-resistant)"										
	/clone_lib="NCI_CGAP_L19"										
Query Match	85.5%;	Score 400.2;	DB 8;	Length 553;							

/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.9 kb. Constructed by Life
 Technologies. Note: this is a NCI_CGAP library."

ORIGIN

Query	Match	Score	DB	Length
Best	Local Similarity	83.9%	2;	771;
Matches	419;	Conservative	Pred. No. 5.1e-101;	
			Mismatches	39;
			Indels	2;
			Gaps	2;
Qy	2			
Db	197	ACTGAGCTGGCTTAGGNGGGACTAGTGAAATGCGCATGCCCTCTCTGGCCAG	61	
Qy	62	CCTGGTGGAGATGPGCAGTACAGGAGCACATGGAGGAGNTGANTGANTCC	121	
Db	257	CTGGTGGAGA-TGTGCGAGTACAGGAGGACACATGGAGGAGNTGAGTGCAGTC	315	
Qy	122	CGNAGCTCANCNCANCGCTACTGNAANGACTCAGENACTNTGACCTNGA	181	
Db	316	CGTAGCTCGGTCAGCTGCTACTGTACGGTTGAGGACTGCTGACCTTRGA	375	
Qy	182	TACCTAGTGCTGCTGCCAACATGNNGACATGGCCATGAGGGAAAGCCCT	241	
Db	376	TACCTAGTGCTGCTGCCAACATGGAGGGATGGCATGGCACATGGGAAGCCCT	435	
Qy	242	TTCACTCTCTGCTCCGAGAACATTCTTNTGATGCCAAAAGAACAGGGAGGT	301	
Db	436	TTCACTCTCTGCTCCGAGAACATTCTTNTGATGCCAAAAGAACAGGGAGGT	494	
Qy	302	AGTGGAGCTGACTACTGATGTCAGAACATTAAGGATCCTTNAAGCTTCATNN	361	
Db	495	AGTGGAGCTGACTACTGATGTCAGAACATTGAGTCATTCCTCAAGCTGGATC	554	
Qy	362	CCAGGGACTGCACTGAGCCAGGTGATGGACCTGGAGAGNCCTGNTATGTC	421	
Db	555	CCAGGGACTGCACTGAGCCAGGTGATGGACCTGGAGGCTGCTGCTGCTG	614	
Qy	422	CCCTGGCTTACCCCTGATGCTGGCTGAGCTGGCTGCTGCTGCTGCTGCTG	461	
Db	615	CCCTGGCTTACCCCTGATGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTG	654	

ORIGIN

Query	Match	Score	DB	Length
Best	Local Similarity	70.3%	6;	750;
Matches	342;	Conservative	Pred. No. 7.8e-83;	
			Mismatches	35;
			Indels	1;
			Gaps	1;
Qy	91	GGACCACTGGGAGNTGNTGNTGNTGANTCCGAGAAGTCAGNCACAGTCTACT	150	
Db	1	GGACCACTGGGAGNTGNTGNTGNTGANTCCGAGAAGTCAGNCACAGTCTACT	60	
Qy	151	GNAGNGACTCAGNAGACTNTGACCTTGATGATACCTTGCTGCTGCTGCTG	210	
Db	61	GTACGGTGTCAAGGAGCTGCTGACCTTGATGACCTTGCTGCTGCTGCTG	120	
Qy	211	NCNATGGCATGACATCGGAAGCCCTTTCAGTCCTCTCCGGCAGACATTC	270	
Db	121	GGCGATGGCAGTGGCAGTGGGAAGGCCCTTTCAGTCCTCTCCGGCAGACATTC	180	
Qy	271	TTTTTTGTGCCCCAAAAGAACAGGGACGGACGGCTAGTGAGTCGCTGACT	330	
Db	181	TTTCITTGATGCCAAGAACAGGGACGGCTAGTGAGTCGCTGACTGATGCG	239	
Qy	331	AATTCAGCCATCTTNAAGCTGGCTATTNCCAGGGACTGNCAGCTGACATG	390	
Db	240	AATTCAGCCATCTTCAAGCTTCATCTCCGAGACTGCGAGTCACCCAGTC	299	
Qy	391	TTGGTAGCTGGAGNCCTGNTATGCTCTCCCTGCTTACCTGATGCTGCTG	450	
Db	300	TTGGTAGCTGGCTCTGCTATGCTCTCCCTGCTTACCTGATGCTGCTG	359	
Qy	451	NCACACCCCTCATGG	468	
Db	360	TCACACCCCTCATGG	377	

RESULT 13

LOCUS	DEFINITION	VERSION	KEYWORDS	SOURCE	ORGANISM
CF726195	CF726195	U1-M-G30-cip-h-06-0-UT.r1	NIH_BMAP_G30	Mus musculus	linear EST
		IMAGE:30606413	5', mRNA sequence.		09-OCT-2003
ACCESSION	CF726195	CF726195.1	GI:37600363		
VERSION			EST.		
KEYWORDS					
SOURCE					
ORGANISM					

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Barchontoglires; Glires; Rodentia; Sciuromorphati; Muridae; Murinae; Mus.

REFERENCE NIH-MGC <http://mgc.ncbi.nih.gov/>
 AUTHORS NIH-MGC
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strauberg, Ph.D.
 Email: cgaps@mail.nih.gov

Tissue Procurement: Dr. James Lin University of Iowa
 DNA Library preparation: Dr. M. Bento Soares, University of Iowa
 DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at
<http://genome.uiova.edu/distribution/mousefl.html>
 This clone was contributed by the Brain Molecular Anatomy Project
 (BMAP)

FEATURES	REFERENCE	COMMENT
source	1.	.750

AUTHORS	NIH-MGC http://mgc.ncbi.nlm.nih.gov/.
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Straubberg, Ph.D. Email: cgapbs-r@mail.nih.gov
FEATURES	cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov
source	Plate: LLNL1:938 Row: 1 column: 13 High quality sequence stop: 628.
FEATURES	Location/Qualifiers
source	1. 628 /organism="Mus musculus" (/db_xref="taxon:10090" /clone="IMAGE:5368788" /tissue_type="retina" /lab_ho="DH10B (phage-resistant)" /clone_id="NIH_MGC_94". Note: this is a NIH_MGC library."
ORIGIN	Query Match 68.6%; Score 321.2; DB 3; Length 628; Best Local Similarity 90.6%; Pred. No. 1.5e-60; Matches 345; Conservative 0; Mismatches 34; Indels 2; Gaps 2;
Qy	88 GAGGGACACTGGGAGNTNTGNTGANTCCGNAGGTCANGNCANCTGTCT 147 Db 1 GAGGGACACTGGGAGNTNTGNTGANTCCGNAGGTCANGNCANCTGTCT 60 Qy 148 ACTGTAAGGTGTTCAAGGACTCTGACCTT-GGATACCTAAGCTGTCTGTCACATTG 207 Db 61 ACTGTAAGGTGTTCAAGGACTCTGACCTT-GGATACCTAAGCTGTCTGTCACATTG 119 Qy 208 NCANCATGCCATCACATCGGAAGACCTTCACTCCCTCCGGCAGAACAT 267 Db 120 TGTGCGATGCGCATGCACTGCACTCGGAAAGCCCTTTCAGCTCCCTCCGGCAAGACAT 179 Qy 268 TGTCTTNTTGATGCCAAAGAAGGGCAAGGTAGTAGTGAGCTGCTGACTCTGATGTGC 327 Db 180 TCTTCTTCTGATGCCAAAGAAGGGCAAGGTAGTAGTGAGCTGACTCTGATGTGC 238 Qy 328 AGAAATTCAAGGCACTCCNTNAGCTTCATATNCCTCCAGGACTGNCAGCTGACCCAGG 387 Db 239 AAGGATTCAAGTCATCCCTCAAGCTGCTCATCTCCAGGACTGCGGAGCTGACCCAGG 298 Qy 388 TGTATTCGTTAGGCCGAGNCCTGNTATGCTCCCTGCTTACCTGATGCTGCTG 447 Db 299 TGTATTCGTTAGGCCGAGNCCTGNTATGCTCCCTGCTTACCTGATGCTGCTG 358 Qy 448 NNGCACACCCGCTCATG 468 Db 359 TGTGTCACACCCGCTCATG 379
FEATURES	Location/Qualifiers
source	1. 4340 /organism="Pongo pygmaeus" (/mol_type="mRNA" /db_xref="taxon:9600" /clone="DKRZp469G0617" /tissue_type="kidney" /clone_id="469" (synonym: phid1). Vector pSport1_SfI; host DH10B; sites SfI1 + SfII1" /dev_stage="adult" /note="AP-binding cassette, sub-family B, member 8, mitochondrial precursor (Homo sapiens)" 1. 4340 /gene="DKRZp469G0617" /gene_id="CAH93981" /codon_start=1 /product="hypothetical protein" /protein_id="CAH93981" /db_xref="GI:55728061" /translation="MLVHLPRVIRGGPPGRLLPLPQFTAVERVSDGYNSSSLFW AVAHLSQWALHPRLPAPRPSAWKQWGGALGPWTSKPHLCLVALCERBAT PASSTPVIGSRTRWKLTWFLRPFLHTGVAVLALGRALVQFLPLGLVTEVA KYTRDHVSFSMTESOSNTSHTHILYVGQULTYGLVLSVBERMVMRFLSSL LRODIAFPANKYQOLVSLRTTVOBPSKFLVTSQGLRSCTVAGCVLSRM8TR LTUMLMLTPPMVGTVTGGSKRLSQDQBLRQVADLGNVTRFQAFRAMEQ REERYGABLBACRBRBRLGJGLSOSLNTAFCNCHVLTGTFPQISLGIVAGQDQTG DLSPLVUSQVSRSMALSVLQVGRGLSAGARVTFMAMPCIPISGQCCVPKBO LRGSVTQVVCFSFSPCRGFKEVLFDTIPKVLGVQVSGGTTVASSLRFYD PTAGGVVMDQDQDRLTDSWMLRQVGFISQEPFLGTTTMEVFGKLEASVEYA AARBNRHTTFRPGTNTVTRGRTLSTVGRGTRVHTRWMDRVRWAGTHBLKK LDABSERVQVQLDRASGRTRVHTRWMDRVRWAGTHBLKK GGIAELTRQRQDAPTAAPLPRKPKPRHRHKRS".
RESULT	15
Qy	Query Match 67.9%; Score 317.6; DB 4; Length 4340; Best Local Similarity 79.1%; Pred. No. 2.5e-79; Matches 367; Conservative 0; Mismatches 96; Indels 1; Gaps 1;
Qy	5 GAGCTGCCCTAGGGGGCACTGAGTGTACAGATCCCTGCTCTGGCCAGCTG 64 Db 482 GAGCTGCCCTAGGGGGCACTGAGTGTACAGATCCCTGCTCTGGCCAGCTG 541 Qy 65 GTGGAGATGTCGCCAGTACAGGGGACACGAGGAGTTCTGGCCAGCTG 124 Db 542 GTAGAGATGTCGCCAGTACAGGGGACACGAGGAGTTCTGGCCAGCTG 601 Qy 125 AAGCTCAGCNCANCTGCTCTACTGAGCTGAGCTGAGCTGCTGCTG 184 Db 602 AATCTGACACCCACCTGCTATCTCTCATGTCAGGACTCTGACTCTGGTAC 661 Qy 185 CTAGTGCTGCTGCCCCACATGNGANCATGGCCATGNACATGGAAAGCCCTTTC 244
ORGANISM	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Pongo Pygmaeus

Db	662	CTGGTGTGCTGTCATGTGGAGGGCATGGCATGGAGGAGCCCTTC	721
Oy	245	AGCTCCCTGCTCGGCAGACATGGCTTNTTGATGCCAAGAACAGGGCAGGTTAGT	304
Db	722	AGCTCCCCTGCTTGACAGAGACATGGCCATTAGACAGGCGAGGCTAGT	780
Oy	305	GATCTGCTTAATGACTGATGTTGAAAGATTCAAGGATCTTNAAGCTTGCAINTNCA	364
Db	781	GAACCGCTTACAACTGACGTCAGGAGGTTAAGTCATCTTCAGCTTGTCATCTCCA	840
Oy	365	GACGACTTGACGACTGNAACCCAGTGATTTGGTAGCCTGAGAGNCCTGNNATACTTGNCACC	424
Db	841	GGGGCTGGGAAGCTGCAACCCAGGTGGCAAGCTTCTGGTCTCTGTCATCTGCTAC	900
Oy	425	TCCCTTACCTGATGCTGGCTGCTGNNGNCAACCCGGCTCTCTG	468
Db	901	ACCCCTCACGCTCTGCTGATGCTGGCCACACGGCCCTATGG	944

Search completed: January 20, 2006, 22:22:46
Job time : 3089 sec

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Copyright GenCore version 5.1.6
(c) 1993 - 2006 Compugen Ltd.

Om nucleic - nucleic search, using sw model

Run on: January 20, 2006, 20:26:08 ; Search time 162 Seconds
(Without alignments)
5135.178 Million cell updates/sec

Title: US-10-327-713-267
Perfect score: 468
Sequence: 1 gactgagtcggccatagg...ngncacaccgcgtcatgg 468

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780928 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/pctodata/1/ina/6B-COMB.seq: *
5: /cgn2_6/pctodata/1/ina/R-COMB.seq: *
6: /cgn2_6/pctodata/1/ina/PCTUS-COMB.seq: *
7: /cgn2_6/pctodata/1/ina/PP-COMB.seq: *
8: /cgn2_6/pctodata/1/ina/RB-COMB.seq: *
9: /cgn2_6/pctodata/1/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	51.8	11.1	1647	Sequence 4211, AP
2	51.8	11.1	21330	Sequence 1209, AP
3	46.4	9.9	1743	Sequence 4073, AP
4	46.4	9.9	24602	Sequence 1202, AP
5	40.8	8.7	9164	Sequence 80, APPI
6	40	8.5	1959	Sequence 4, APPI
7	8.5	8.5	2061	Sequence 17, APPI
8	36.8	7.9	897	Sequence 37, APPI
9	36.2	7.7	1272	Sequence 2685, AP
10	36.2	7.7	1812	Sequence 1526, AP
11	36.2	7.7	1848	Sequence 495, APP
12	36.2	7.7	7760	Sequence 63, APP
13	35	7.5	921	Sequence 5880, AP
14	35	7.5	9574	Sequence 1043, AP
15	34.8	7.4	1800	Sequence 2972, AP
16	34.8	7.4	2133	Sequence 1527, AP
17	34.8	7.4	165651	Sequence 1303, A
18	34.6	7.4	601	Sequence 1787, AP
19	34.6	7.4	601	Sequence 5940, AP
20	34.6	7.4	33821	Sequence 613, APP
21	34.6	7.4	33822	Sequence 737, APP
22	34.4	7.4	1168	Sequence 137, APP
23	34.4	7.4	1168	Sequence 143, APP
24	34.2	7.3	US-09-973-298-143	Sequence 10804, A
25	34.2	7.3	US-09-252-991A-10228	Sequence 10228, A
26	34.2	7.3	US-09-252-991A-10345	Sequence 10345, A
27	34.2	7.3	US-09-902-540-8140	Sequence 8140, AP
28	34.2	7.3	US-09-711-619-8	Sequence 8, APPI
29	34.2	7.3	US-09-902-540-754	Sequence 754, APP
30	34.2	7.3	US-09-711-619-7	Sequence 7, APPI
31	34.2	7.3	US-09-902-540-834	Sequence 834, APP
32	33.8	7.2	1800	Sequence 5879, AP
33	33.6	7.2	1995	Sequence 9307, AP
34	33.6	7.2	10092	Sequence 994, APP
35	33.5	7.2	13637	Sequence 1097, AP
36	33.4	7.1	219	Sequence 3135, AP
37	33.4	7.1	601	Sequence 157317, AP
38	33.4	7.1	753	Sequence 86, APPI
39	33.4	7.1	2486	Sequence 4392, AP
40	33.4	7.1	12061	Sequence 16134, A
41	33.4	7.1	105519	Sequence 1, APPI
42	33.2	7.1	608	Sequence 8803, AP
43	33.2	7.1	71	Sequence 6825, AP
44	33.2	7.1	1272	Sequence 569, APP
45	33.2	7.1	4407	Sequence 1, APPI

ALIGNMENTS

RESULT 1
US-09-902-540-4211
; Sequence 4211, Application US/0902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wieand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-1015849B
; CURRENT APPLICATION NUMBER: US/09/902-540
; CURRENT FILING DATE: 2001-07-10
; PRIORITY APPLICATION NUMBER: 60/217,883
; PRIORITY FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO: 4211
; LENGTH: 1647
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; US-09-902-540-4211

Query Match Best Local Similarity 11.1%; Score 51.8; DB 3; Length 1647;
Matches 181; Conservative 0; Mismatches 229; Indels 1; Gaps 1;

QY 53 CTGGCCACCTGGAGGAGATGGCGCAAGTACAGCGGACCATGGAGGNTNCNG 112
Db 19 CTGGCCCTATCCCCGCCCTATGGCGACCTGGGACCACTGGCGCCCTACCCGGCGAACCG 78
QY 113 TTTGAGTCCGNAAGCTCAGCNCAGNCAGCTCTACTGAGACAGTCAGGAGCTGNG 172
Db 79 TATGGGTGACCGCGTCGGATCTGAGCTGGCTCCGGCATCGCC 138
QY 173 ACCTTGATACCTAGTGGCTGCCACATTGNNANCACTGGCTTGTGAGTGGCGCG 232
Db 139 ATGGCGCTGGCATCTACCTCTGACACAGCGCGGAACGCGTGTGCGSGCTGCSC 198
QY 233 AAAGCCCTTTCACCTCCCTGCTGGCGAAGACATTGCTTNTTGTGCCAAAGACA 292
Db 199 AAGGACCTTCGGCCCTGGCTCCAGGAGCTGGCTTCTGGATGGCGCG 258
QY 293 GGGCGCGTGTGAGTCGTCTACTGAGTGTGCAAGGATTCAGGCATCTTNAAGCT 352
Db 259 GGCGAGCTCACC-ACCGCGCTCTCTGGACACACCGCTGCGACACCGTCACGGC 317
QY 353 TGTCAINTNCCAGGGACTGNGCAGCTGNACCCAGGTATGGTAGCTGGAGNCCTGNN 412

RESULT 2
US-09-902-540-1209/C
Sequence 1209, Application US/09902540
; Patent No. 6833447

GENERAL INFORMATION:

APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.

TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof

FILE REFERENCE: 38-10(15849)B

CURRENT APPLICATION NUMBER: US/09/902,540

CURRENT FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: 60/217,883

PRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825

SEQ ID NO: 1209
LENGTH: 21330
TYPE: DNA
ORGANISM: Myxococcus xanthus

FEATURE:
NAME/KEY: unsure
LOCATION: (1)-(21330)
OTHER INFORMATION: unsure at all n locations

US-09-902-540-1209

Query Match 11.1%; Score 51.8; DB 3; Length 21330;
Best Local Similarity 44.0%; Pred. No. 5.3e-05; Mismatches 229; Indels 1; Gaps 1;
Matches 181;

QY 53 CTGGGCCAGCTGGAGATGTCGCCAGATACAGCACCGGGGACCTTGAGGAGNTNCNTG 112
Db 18612 CTGGCCTATCCGGGCCATTGGCACCTGGTGGACCGCTCACCGGGCGACGG 18553

QY 113 TTTGANTCCCGAAAGCTCANCNCANCTGTGCTACTGAGNAGCTTCAGNACTGNTG 172
Db 18552 TATGTGGTGGACGGCTGCGGATGTCATGCTGGCTGTCAGGTGCAAGCATGCC 18493

QY 173 ACCTTNGATACTTGTGCTGGTCCACATGGNNANCATGGCATACATGCGG 232
Db 18492 ATGGCCTTGCGCATCTACCTTTCACCAACCGGGGAACCGCTGGTCCGGTGGC 18433

QY 233 AAAGCCCTTTCAGTCCTCTGTCGGAAACATTCCTTNTTGATGCCAAAGACA 292
Db 18432 AAGGACCTCTGGGGCTGTCGGACCTGGTGGCTCTCGATCCGGCCACG 18373

QY 293 GGGCAGSGTAGTGAGTGCTGACTACTGAGTCAGAAGATCAAGCACTTNAAGT 352
Db 18372 GGCGAGCTCACC-AGCGCGCTCTCTGGACGACACCGTCAAGGC 18314

QY 353 TGTCAATNCAGGGACTGNGCAGTGACCCAGGTAATGTTAGCTGGAGNCCGN 412
Db 18313 CAAGCTGTCAGTATGCTGCGCTACAGTGAGTGGTGGCTACCCCGT 18254

QY 413 TATGCTGNCCTCGCCTAACCTGATGCTGCTGCTGNGNCAACCGGCCCT 463
Db 18253 CTACACCTCGCAGCTCACCTGGTGGATGTCGGCTCATCCCGT 18203

RESULT 4
US-09-902-540-1202
Sequence 1202, Application US/09902540
; Patent No. 6833447

GENERAL INFORMATION:

APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.

TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof

FILE REFERENCE: 38-10(15849)B

CURRENT APPLICATION NUMBER: US/09/902,540

CURRENT FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: 60/217,883

PRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825

SEQ ID NO: 4073
LENGTH: 1743
TYPE: DNA
ORGANISM: Myxococcus xanthus

US-09-902-540-4073

Query Match 9.9%; Score 46.4; DB 3; Length 1743;
Best Local Similarity 48.5%; Pred. No. 0.0024; Mismatches 134; Indels 1; Gaps 1;
Matches 127;

QY 206 GNGNANCATGGCATGACATGGGAAGGCCCTTCAGCTCCCTGTCGGCAAGAC 265
Db 7290 GGTGAGGCGATGTCAGGACCTGGGAGCGCTGATGCGACCTTGCTGGAGGAG 7349

QY 266 ATTGCTTNTTGATGCCAAAGACAGGAGCTAGTGAGTCGCTTGACTACTGATG 324

STREET: 130 Bishop Allen Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: United States of America
ZIP: 02139

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44Mb storage
OPERATING SYSTEM: Windows 95
SOFTWARE: Microsoft Word 97 SR-1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/061,764A
FILING DATE: April 16, 1998
CLASSIFICATION: 424
PRIORITY APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Yankwich, Leon R.
REGISTRATION NUMBER: MGH-002.0 US/MHG-1247.0
TELECOMMUNICATION INFORMATION:
REFERENCE DOCKET NUMBER: MGH-002.0 US/MHG-1247.0
TELEPHONE: 617-491-4343
TELEFAX: 617-491-8801

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
LENGTH: 1959 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: Synthetic DNA fragment

US-09-814-915A-80

Query Match 8.7%; Score 40; DB 3; Length 9164;
Best Local Similarity 43.8%; Pred. No. 0.078;
Matches 126; Conservative 0; Mismatches 162; Indels 0; Gaps 0;

QY 8 CTGGCTTAGGTGCCACTAGTGAATGCGAGATCCCTGCTGCCTGAGCAACCTGG 67
Db 6523 CTGGCCAGTGCGGTGTCATGGAGGCCCTGACCCCTGGCCGGCTGGC 6582
QY 68 GAGATGTGCCAACATGACAGGAGGACACATGGAGGAGNTCTNTGANTCCGNAAG 127
Db 6583 CTGCAAGACCCAAAGGACCTCTGGCTGAGGGAGCTGGAGAGACAGGACCTCCAG 6642

QY 128 CTCANCGNCANCCTCTCTRACTGAGNAGTGGTCAAGNACTGNTGACCTTNGGATACCTA 187
Db 6643 GACGGCGCTGACTGGACTTGTGGACTCTGGACCTCCGGCCCTTCAG 6702

QY 188 GTGCTCTGTCGCCAACATGGNGANNCATGCCATGACATGGGAAAGCCCTTTCAG 247
Db 6703 GCCTGTGGTCCACAGGGTCTCCAGGTGTGCCAGTGGAGACAGTGGGAGACAGG 295
QY 248 TCCCTCTCCGGCAAGAACATGTGCTTNTTGATGCAAAGAACGG 6810
Db 6763 CGGGAAAGCCCAAGTCGAGATGTGCCAGTGGAAAGATGGAGACAGGAG 6810

RESULT 6
US-09-814-915A-80

Sequence 80, Application US/09814915A
Patent No. 6750015

GENERAL INFORMATION:
APPLICANT: Horwitz, Kathryn
TITLE OF INVENTION: Progesterone Receptor-Regulated Gene Expression and Methods Relat
TITLE OF INVENTION: Thereto
FILE REFERENCE: 2848-39

CURRENT APPLICATION NUMBER: US/09/814,915A
CURRENT FILING DATE: 2002-03-21
PRIOR APPLICATION NUMBER: 60/214,870

PRIOR FILING DATE: 2000-06-28

NUMBER OF SEQ ID NOS: 108

SOFTWARE: PatentIn version 3.1

SEQ ID NO: 80
LENGTH: 9164
TYPE: DNA
ORGANISM: Homo sapiens

US-09-814-915A-80

Query Match 8.7%; Score 40; DB 3; Length 9164;
Best Local Similarity 43.8%; Pred. No. 0.078;
Matches 126; Conservative 0; Mismatches 162; Indels 0; Gaps 0;

QY 198 CCCACATTGNNGANNCATGGCATGNAATGGGAAAGCCCTTCACTCCCTGCTCC 257
Db 644 CCTACACCATGTCGAATCACTGGGAATCCGGAGAGCTTCTCTCCCTGCTC 703

QY 258 GGCGAGACATTGCTTNTTGATGCCAAGAACAGGAGGAG 299
Db 704 GCCAGGACCTGGTCTCCAGGAGACTTAAGACAGGGAGAC 745

RESULT 7
US-09-061-764A-17

Sequence 17, Application US/09061764A
Patent No. 6284879

GENERAL INFORMATION:
APPLICANT: Faustman, Denise L
TITLE OF INVENTION: TRANSPORT ASSOCIATED PROTEIN SPLICER VARIANT
TITLE OF INVENTION: AND MODEL FOR IMMUNE DIVERSITY

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:
ADDRESSEE: Yankwich & Associates
STREET: 130 Bishop Allen Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: United States of America
ZIP: 02139

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44Mb storage
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Microsoft Word 97 SR-1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/061,764A
FILING DATE: April 16, 1998
CLASSIFICATION: 424

PRIOR APPLICATION DATA:

RESULT 6
US-09-061-764A-4

Sequence 4, Application US/09061764A
Patent No. 6284879

GENERAL INFORMATION:
APPLICANT: Faustman, Denise L
TITLE OF INVENTION: TRANSPORT ASSOCIATED PROTEIN SPLICER VARIANT
TITLE OF INVENTION: AND MODEL FOR IMMUNE DIVERSITY

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:
ADDRESSEE: Yankwich & Associates
STREET: 130 Bishop Allen Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: United States of America
ZIP: 02139

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44Mb storage
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Microsoft Word 97 SR-1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/061,764A
FILING DATE: April 16, 1998
CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 10/674,177
FILING DATE: 03-12-2003
ATTORNEY/AGENT INFORMATION:
NAME: Yankwich, Leon R.
REGISTRATION NUMBER: 30,237
REFERENCE/DOCKET NUMBER: MGH-002.0 US/MHG-1247.0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-491-4343
TELEFAX: 617-491-8801
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 2061 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: synthetic DNA fragment

Sequence 2685 Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al.
TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
PRUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709_2004001
CURRENT APPLICATION NUMBER: US/09/489, 039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117, 747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO: 2685
LENGTH: 1272
TYPE: DNA
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-3685

RESULT 8
US-09-303-518D-37

GENERAL INFORMATION:
PATENT NO.: 6914131
APPLICANT: Scarlato, Vincenzo
APPLICANT: Masignani, Vega
APPLICANT: Rappoli, Rino
APPLICANT: Pizza, Mariagrazia
APPLICANT: Grandi, Guido
TITLE OF INVENTION: *Nasibrial Antigens*
FILE REFERENCE: CHIRO160
CURRENT APPLICATION NUMBER: US/09/303,5
CURRENT FILING DATE: 1999-04-30
NUMBER OF SEQ ID NOS: 1098
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 37
LENGTH: 897
TYPE: DNA
ORGANISM: *Neisseria gonorrhoeae*
US-09-303-518D-37

Query Match	7.9%; Score 36.8; DB 3; Length 897;
Best Local Similarity	50.0%; pred. No. 0.46;
Matches	83; Conservative 0; Mismatches 83; Indels 0; Gaps 0
Oy	181 ATACCTAGTGTGTCATGCCACATTTGGANGANCNCATGCGCCATGCGGAAGACCCCT 240
Db	707 ATACCGGGGGGGCTTGCCCAACCGGAATTGCGCTGCCCGCAAGGGCGAACATGATG 766
Oy	241 TTTCAGCTCTGCTCCGAGAGATTGCTTNTTGATGCCAAAGAGCAGGCAGCG 300
Db	167 CCGCCGCCAACCGTCCGGGAAATACTCTGTTATTCGTTCCAAATGGACGGCACGG 826
Oy	3.01 TAGTAGTGCCTGTGACTGTGAGAAGATTAGGGATCTT 346
Db	827 GCTTAGGCCAGTTCAGCCATGATTGACCGAACACAGCGCGCTT 872

RESULT 9
US-09-489-039A-2685

RESULT 11
US-03-107433-495
; Sequence 495, Application US/09107433
Patent No. 6300744

GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGNOSTIC THERAPEUTICS

NUMBER OF SEQUENCES: 5206

CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02454

COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: <Unknown>
OPERATING SYSTEM: <Unknown>

SOFTWARE: <Unknown>

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433

FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/ 085131

FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/051553

FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:
NAME: Arinello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-011
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007

INFORMATION FOR SEQ ID NO: 495:
SEQUENCE CHARACTERISTICS:
LENGTH: 1848 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Streptococcus pneumoniae

FEATURE:
NAME/KEY: mlbc feature
LOCATION: (B) LOCATION 1...1848
SEQUENCE DESCRIPTION: SEQ ID NO: 495;

US-03-107433-495

Query Match 7.7%; Score 36.2; DB 3; Length 1848;
Best Local Similarity 46.6%; Pred. No. 0.95; Mismatches 131; Indels 1; Gaps 1;
Matches 115; Conservative 0; Mismatches 131; Indels 1; Gaps 1;

RESULT 12
US-03-961-527-63
; Sequence 63, Application US/08961527
Patent No. 6420135

GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391

CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527

FILING DATE:
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-5504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 7760 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-961-527-63

Query Match 7.7%; Score 36.2; DB 3; Length 7760;
Best Local Similarity 46.6%; Pred. No. 1.8; Mismatches 131; Indels 1; Gaps 1;
Matches 115; Conservative 0; Mismatches 131; Indels 1; Gaps 1;

Db 308 GTCTCTGAGCCGGCGTGTATCGAGACCAACCGAGATCGCAAAGGCCTCTTGTA 367
Db 249 CCCCTCTCCGCGAAGCATCTTGTATGCCAAAGAACAGCGCAGCTAGT 308
Db 368 AGCTCTCTACTGATGCGAAGATTCAAGGCATCTTNAAGCTCTCATNTNCAGGA 368
Db 427 CATTTCACCTGATTGGATAATCTACAGCCTTACAGAAGCTGTGATTCAGGTC 485
Db 369 CTGNGCA 375
Db 487 ATGAGCA 493

Qy 129 TCGACGNCCANCCTCTCTACTGATGAGACTGTTAGGACTCTTGTGATATACATG 188
Db 284 TCTATGTCATCTCTGGCCCTCTGGTTGTTCTATTATCTCTAGT 343
Qy 189 TGCCTCTGCCCCACTTGTGAGACAGCTGATGCCATGCGATATCCGTCT 426
Db 344 GTCTCATGAGCGGGGTGATGAGATGCCAACAGAGAGACAGGGCGCGTAGT 403
Db 249 CCCCTCTCCGCGAACATCTGCTTNTGATGCCAAAGAACAGCGCAGCTTCAGCT 308
Db 404 AGCTCTCTACTGATGCGAAGATTCAAGGCATCTTNAAGCTGTGATTCAGGTC 462
Db 309 CGCTGACTACTGATGCTGAGAACTCAAGGCATCTTNAAGCTGTGATTCAGGTC 368
Db 463 CATTTCACCTGATTGGATAATCTACAGCCTTACAGAAGCTGTGATTCAGGTC 522
Qy 369 CTGNGCA 375
Db 523 ATGAGCA 529

QY 5718 GTCMCTCATGAGCGGGTGTGATTGCGAGATGCCAACAGGAGATGGGAGCTAGTACTG 5777

QY 249 CCCCTGCTCCGGCAAGAAGATGCTTTTGATGCCAAGAACAGGAGCTAGTACTG 308

Db 5778 AGCTTGCTCAGTGTGAGCGGTTCTTCTTGA -CGCTGCAAGATGGCATATTCCTGCT 5836

QY 309 CGCTTGACTACTGATGTCAGAAATCTCAAGGCATCTTAAAGGAAACCTGATTCAGGGA 368

Db 5837 CATTTACCACTGATTGATAATTCTCAAGCTTAAAGGAAACCTGATTCAGGGA 5896

QY 369 CTGNGCA 375

Db 5897 ATGAGCA 5903

RESULT 13

US-09-902-540-5880 Application US/09902540

PATENT INFORMATION:

APPLICANT: Goldman, Barry S.

APPLICANT: Hinke, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Wiegand, Roger C.

TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof

FILE REFERENCE: 38-10(15449)B

CURRENT APPLICATION NUMBER: US/09/002,540

CURRENT FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: 6833447

PRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825

SEQ ID NO 5880

LENGTH: 921

TYPE: DNA

ORGANISM: Myxococcus xanthus

US-09-902-540-5880

Query Match 7.5%; Score 35; DB 3; Length 9574;

Best Local Similarity 50.7%; Pred. No. 4.5; Mismatches 0; Indels 0; Gaps 0; Matches 68; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

OTHER INFORMATION: unsure at all n locations

US-09-902-540-1043

Query Match 7.5%; Score 35; DB 3; Length 9574;

Best Local Similarity 50.7%; Pred. No. 4.5; Mismatches 0; Indels 0; Gaps 0; Matches 68; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

OTHER INFORMATION: unsure at all n locations

US-09-212-991A-2972

Sequence 2972, Application US/09252991A

PATENT NO. 6551-95

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

FILE REFERENCE: 10716-136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 2972

LENGTH: 1802

TYPE: DNA

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-2972

Query Match 7.4%; Score 34.8; DB 3; Length 1800;

Best Local Similarity 48.1%; Pred. No. 2.5; Mismatches 81; Indels 0; Gaps 0; Matches 75; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

OTHER INFORMATION: unsure at all n locations

US-09-902-540-1043/C

Sequence 1043, Application US/09902540

PATENT NO. 6833447

GENERAL INFORMATION:

APPLICANT: Goldman, Barry S.

APPLICANT: Hinke, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Wiegand, Roger C.

TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof

FILE REFERENCE: 38-10(15449)B

CURRENT APPLICATION NUMBER: US/09/002,540

PRIOR APPLICATION NUMBER: 6833447

PRIOR FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: US/09/902,540

NUMBER OF SEQ ID NOS: 16825

SEQ ID NO 1043

LENGTH: 9574

TYPE: DNA

Search completed: January 20, 2006, 22:25:29

Job time : 165 sec

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 20, 2006, 20:33:00 ; Search time 657 seconds
(without alignments)
5890.516 Million cell updates/sec

Title: US-10-327-713-267
Perfect score: 468
Sequence: 1 gactgagctggcccttaaggtagt.....ngacacccgcctcatgg 468

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues
Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 0

Post-processing: Minimum Match 0%
Maximum Match 100%

listing first 45 summaries

Database : Published Applications NA Main.*

1: /cgtr2_6/ptodata/1/pubprna/us07_prcomb.seq: *
2: /cgtr2_6/ptodata/1/pubprna/us08_prcomb.seq: *
3: /cgtr2_6/ptodata/1/pubprna/us09a_prcomb.seq: *
4: /cgtr2_6/ptodata/1/pubprna/us09b_prcomb.seq: *
5: /cgtr2_6/ptodata/1/pubprna/us10a_prcomb.seq: *
6: /cgtr2_6/ptodata/1/pubprna/us10b_prcomb.seq: *
7: /cgtr2_6/ptodata/1/pubprna/us10c_prcomb.seq: *
8: /cgtr2_6/ptodata/1/pubprna/us10d_prcomb.seq: *
9: /cgtr2_6/ptodata/1/pubprna/us11_prcomb.seq: *
10: /cgtr2_6/ptodata/1/pubprna/us11_prcomb.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No:	Score	Query Length	DB ID	Description
1	316	67.5	2392	US-10-108-260A-258
2	316	67.5	2417	US-09-823-2640A-601
3	219.6	46.9	1805	US-10-264-237-516
4	206.8	44.2	494	US-09-918-995-0941
5	127.8	27.3	423	US-10-263-828-64
6	117.6	25.1	425	US-09-918-995-34259
7	93	19.9	2379	US-11-097-143-2507
8	93	19.9	4940	US-11-097-143-2506
9	74	15.8	283	US-09-764-891-2676
10	74	15.8	555	US-10-091-572-214
11	11.8	574	6	US-10-264-337-718
12	11.1	1773	6	US-10-369-993-43142
13	9.9	1773	6	US-10-369-993-43123
14	4.4	434	8	US-10-357-930-30101
15	4.4	483	8	US-10-357-930-43584
16	4.4	607	5	US-10-123-572-344
17	4.0	607	6	US-10-146-731-344
18	4.0	607	6	US-10-140-472-344
19	4.0	607	6	US-10-141-611-344
20	4.0	607	6	US-10-142-885-344
21	4.0	607	6	US-10-158-90-344
22	4.0	607	6	US-10-137-871-344
23	4.0	607	6	US-10-137-871-344

RESULT 1
US-10-108-260A-258
; Sequence 258, Application US/10108260A
; Publication No. US2004005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: FILE REFERENCE: HI-A0105
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO: 258
; LENGTH: 2392
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-108-260A-258

Query Match

Best Local Similarity 67.5%; Score 316; DB 6; Length 2392;
Matches 366; Conservative 78.9%; Pred. No. 7.1e-96; Mismatches 97; Indels 1; Gaps 1;

ALIGNMENTS

QY 5 GAGCTGCGCTTATGGCGCACTAGTAGATGTCAGGCCCTTGCTCTGCGCCAGCTG 64
Db 428 GTGCCTGGCCGCTGGCTGGCGACTCTGTGATGAGATCCTCCCTGCTCTGGCCAGCTG 487
QY 65 GGGAGATGTTGGCACTACAGCAGGACACTGGGGAGNTGNTGANTCCTCC 124
Db 488 GTAGAGGTGTGCGCAAGTACAGCAGGAGCTGGAGGTTCATGACTGACTCCAG 547
QY 125 AAGCTCTGGCCGCACTGCTCTACTGAGCTGAGCTGAGCTTCAAGNACTGTA 184
Db 548 ATCTGGACCCACTGTCTTCTCTATGGCTCAGGACTGCTGACCTTCTGGCTG 607
QY 185 CTAGCTGCTGCTGCCACATGGGAGNCATGCCATAGCTGGAAAGCCCTTTC 244
Db 608 CTGGCTGCTGCTGCCACGTGGCTGGAGCTGGCTGAGCATGGAGGGCCCTCTC 667
QY 245 AGCTCCCTGCTGCCACATGGGAGNCATGCCATAGCTGGAAAGCCCTTTC 304
Db 668 AGCTCCCTGCTGCCACATGGCTGGCTGGAGCTGGCTGAGCATGGAGGGCCCTCTC 726
QY 305 GAGTGTGCTGACTACTGATGCTGGAGAACTCAAGGCCATCTTNAAGCTGTCATNNCCA 364
Db 727 GGGCGCTTGCACTGACTGAGCTGGAGTTAGTCCTCAGCTGCACTCCCA 786

RESULT 2
US-09-823-245A-601
; Sequence 601, Application US/09823245A
; Publication No. US20020039760A1
; GENERAL INFORMATION:
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fechtel, Kim
; APPLICANT: Agostino, Michael J.
; APPLICANT: Howes, Steven H.
; APPLICANT: Resnick, Richard J.
; APPLICANT: Graham, James R.
; ATTORNEY: Genetics Institute, Inc.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
; FILE REFERENCE: GIN 6401
; CURRENT APPLICATION NUMBER: US/09/823, 245A
; CURRENT FILING DATE: 2001-03-29
; PRIORITY APPLICATION NUMBER: 60/154, 941
; PRIORITY FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 631
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 601
; LENGTH: 2417
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (254) .. (254)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (313) .. (313)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (427) .. (427)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (430) .. (430)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1803) .. (1803)
; OTHER INFORMATION: n equals a,t,g, or c
; US-10-264-237-516
Query Match 67.5%; Score 316; DB 3; Length 2417;
Best Local Similarity 78.9%; Pred. No. 7, 1e-96;
Matches 366; Conservative 0; Mismatches 97; Indels 1; Gaps 1;
QY 5 GAGCTGCGCTTGGTGGCGACTCTGTGATATGACAGTCCTCCCTGTCTGGCCAGTG 64
Db 453 GTCCTGGCGCTTGGTGGCGACTCTGTGATATGACAGTCCTCCCTGTCTGGCCAGTG 512
Qy 65 GGGAGATGTCGCCAGTACAGCAGGACCATGGGAATNCAGTGTGANTCCGN 124
Db 513 GTGAGGGTGTGGCCAGTAACAAAGGGACAGCTGAGTCAG 572
Qy 125 AAAGCTCAGNCANCAGCTCTACTGAGNACAGTGGTCAAGGAGCTGAGCTTGGATAC 184
Db 573 AATCTCAGCACCCACCTGTTATCTCTATGGTCAGGACTGCGACCTTCGGTAC 632
Qy 185 CTAGTGCCTGCTGCCACATTGNGANCATGCGCATGACGCCCTTC 244
Db 633 CTGGTGCCTGCTGCCAGGTGGCTGGAGGGCTTGCTGGAGATGGGGAGGCCCTTC 692
Qy 245 AAGCTCCCTGCTGCCAGAACATGCGCTTNTTGATGCCAAAGGAGGCGAGCTGAGT 304
Db 693 AAGCTCCCTGCTGCCAGAACATGCGCTTNTTGATGCCAAAGGAGGCGAGCTGAGT 751
Qy 305 GAGTCGCTGACTACTGATGAGGAGATCAGGATCCTTNAAGCTGTCAINTNCA 364
Db 752 GAGGCGCTGCTGCCAGAACATGCGCTTNTTGATGCCAAAGGAGGCGAGCTGAGT 811
Qy 365 GAGACTGCGAGCTGAGCCAGCTGATGTTGAGCTGGAGCTGGAGCTGGAGCTGG 424
Db 812 GGGCTGCGAGGTGACCCAGGGTGGAGGCTCCTGTCGTCATCTGTGAC 871
Qy 425 TGCCTTACCTGATGCTGCTGAGTGGCGACACCCGCGCTCTGG 468
Db 872 AGGCTCAGCTGCTGCTGAGTGGCGACACCCGCGCTCTGG 915
; RESULT 3
US-10-264-237-516
; Sequence 516, Application US/10264237
; Publication No. US20040009491A1
; GENERAL INFORMATION:
; APPLICANT: Birbe et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131P1
; CURRENT APPLICATION NUMBER: US10/264, 237
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205, 515
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO: 516
; LENGTH: 1805
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (254) .. (254)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (313) .. (313)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (427) .. (427)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (430) .. (430)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1803) .. (1803)
; OTHER INFORMATION: n equals a,t,g, or c
; US-10-264-237-516
Query Match 46.9%; Score 219, 6; DB 6; Length 1805;
Best Local Similarity 75.8%; Pred. No. 2.9e-63;
Matches 263; Conservative 0; Mismatches 83; Indels 1; Gaps 1;
Qy 122 CGNAAGCTCAGNCANCAGCTGCTCTCTATGAGNACAGTGGAGCTTGGAGA 181
Db 1 CAGAATTCAGCACCCACCTCTTATCTCTATGGTCAGGACTGCGACCTTCGG 60
Qy 182 TACCTAGTGCCTGCTGCCACATTGNGANCATGCGCATGACGCCCT 241
Db 61 TACCTGGTGCCTGCTGCCACATTGNGANCATGCGCATGACGCCCT 120
Qy 242 TTCACTTCTCGCAAGACATGCTTNTTGATGCCAAAGGAGGCGAGT 301
Db 121 TTCACTTCTCGCAAGACATGCTTNTTGATGCCAAAGGAGGCGAGT 179
Qy 302 ATGAGACTGCGCTGACTACTGATGTCAGGAGCTTGGAGCTGGAGCTGG 361
Db 180 GGTGAGCCGCTGACACTGAGTGGAGGAGTTAATGTCATCTCAAGCTGTGAC 239
Qy 362 CCAGGAGCTGCGAGCTGAGCCAGTGTGAGCTGGAGAGNCCTGNTATGTC 421
Db 240 CCAGGAGCTGCGAGCTGAGCCAGTGTGAGCTGGAGGCTGCTGTCATCTGTG 299
Qy 422 CCTCCGCTTACCTGATGCTGCTGAGTGGCGACACCCGCGCTCTGG 468
Db 300 GACACCGCTCACGNCCTGCTGCTGAGTGGCGACACCCGCGCTCTGG 346
; RESULT 4

us-09-918-995-30941
; Sequence 30941, Application US/09918995
; Publication No. US0030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918, 995
; CURRENT FILING DATE: 2001-07-30
; PRIORITY APPLICATION NUMBER: US/09/235, 076
; PRIORITY FILING DATE: 1999-01-20
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO. 30941
; LENGTH: 494
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: misc_feature
; NAME/KEY: misc_feature
; LOCATION: (1)..(494)
; OTHER INFORMATION: n = A,T,C or G
; US-09-918-995-30941

Query Match 44.2%; Score 206.8; DB 3; Length 494;
Best Local Similarity 80.1%; Pred. No. 3..7e-59; Mismatches 0; Indels 0; Gaps 0;
Matches 229; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

Qy 5 GAGCTGGCTTAGTGCAGCACTAGTGAATGTCAGAGATCCCTTGCTCTGGCCACTG 64
Db 208 GTCCTGGCTTGCGCAGCTGTGAAATGACGATGCTGAGCTGGTACCTGGTACCTGTCCTGCGC 202
Qy 65 GTGAGGATGTCGCCAACGTAACAGGGACACATGGGGAGNTNCNTNTGANTCCGN 124
Db 268 GTAGAGGTGCGGCCAACGATCACAGGGACACAGGGAGCTAGCTGGTTCATGACTGAGTCCAG 262
Qy 125 AAGCTCANCNCANCTGCTTACTGNAANGAGTCAGGACTGACTTGGATA 184
Db 328 AACCTCAGCACCCACCTGCTATCTCTATGGTCAGCTGACTGGTAC 387
Qy 185 CTAGTGTCTGGTCCACATGNGANCATGCCATAGCCATGCGAAAGCCCTTC 244
Db 388 CTGTCGTCCTGTCACCTGGCGAGCATGCTTNTGATGCCAANAAA 290
Qy 245 AGCTCCCTGTCGCCAACGATGCTTNTGATGCCAANAAA 290
Db 448 AGCTCCCTGTCGCCAACGACATGCTTNTGATGCCAATGAA 493

RESULT 5
US-10-079-623-212
; Sequence 212, Application US/10079623
; Publication No. US2002016302A1
; GENERAL INFORMATION:
; APPLICANT: Harvukka, Ilkka J.
; APPLICANT: Glenn, Matthew R.
; APPLICANT: Grigor, Murray R.
; APPLICANT: Molenaar, Adrian J.
; TITLE OF INVENTION: Compositions isolated from bovine mammary gland and methods for their use.
; FILE REFERENCE: 11000..1044Ucon
; CURRENT APPLICATION NUMBER: US/10/263, 828
; CURRENT FILING DATE: 2002-10-02
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO. 64
; LENGTH: 423
; TYPE: DNA
; ORGANISM: Bovine
; US-10-263-828-64

Query Match 27.3%; Score 127.8; DB 6; Length 423;
Best Local Similarity 72.5%; Pred. No. 2e-32; Mismatches 57; Indels 0; Gaps 0;
Matches 150; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

Qy 83 TACAGGGGACCATGGGGAGNTNTGANTCCGNAGCTCANCNCANCTG 142
Db 1 TACAGGGGACCATGGGGAGNTNTGANTCCGNAGCTCANCNCANCTG 60

Query Match 27.3%; Score 127.8; DB 5; Length 423;
Best Local Similarity 72.5%; Pred. No. 2e-32; Mismatches 57; Indels 0; Gaps 0;
Matches 150; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

Qy 143 CTCTCTACTGAGCTGAGTCAGGAGACTGTCAGCTTGAGCTGCTGTCCTGCGC 202
Db 61 CTCTCTACTGAGCTGAGTCAGGAGACTGTCAGCTTGAGCTGCTGTCCTGCGC 120

Qy 203 ATTCGGGAGCATGGGTGAGTCAAGGAGGGCTTTCAGCTGCTCTGCGCAA 262
Db 121 ATTCGGGAGCATGGGTGAGTCAAGGAGGGCTTTCAGCTGCTCTGCGCAA 180

Qy 263 GACATTGCTTNTGATGCCAANAAA 289
Db 181 GACATTGCTTNTGATGCCAANAAA 207

RESULT 6
US-10-263-828-64
; Sequence 64, Application US/10263828
; Publication No. US0030138955A1
; GENERAL INFORMATION:
; APPLICANT: Havukka, Ilkka J.
; APPLICANT: Glenn, Matthew R.
; APPLICANT: Grigor, Murray R.
; APPLICANT: Molenaar, Adrian J.
; TITLE OF INVENTION: Compositions isolated from bovine mammary gland and methods for their use.
; FILE REFERENCE: 11000..1044Ucon
; CURRENT APPLICATION NUMBER: US/10/263, 828
; CURRENT FILING DATE: 2002-10-02
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO. 64
; LENGTH: 423
; TYPE: DNA
; ORGANISM: Bovine
; US-10-263-828-64

Query Match 27.3%; Score 127.8; DB 5; Length 423;
Best Local Similarity 72.5%; Pred. No. 2e-32; Mismatches 57; Indels 0; Gaps 0;
Matches 150; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

Qy 83 TACAGGGGACCATGGGGAGNTNTGANTCCGNAGCTCANCNCANCTG 142
Db 1 TACAGGGGACCATGGGGAGNTNTGANTCCGNAGCTCANCNCANCTG 60

Query Match 27.3%; Score 127.8; DB 5; Length 423;
Best Local Similarity 72.5%; Pred. No. 2e-32; Mismatches 57; Indels 0; Gaps 0;
Matches 150; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

Qy 143 CTCTCTACTGAGCTGAGTCAGGAGACTGTCAGCTTGAGCTGCTGTCCTGCGC 202
Db 61 CTCTCTACTGAGCTGAGTCAGGAGACTGTCAGCTTGAGCTGCTGTCCTGCGC 120

Qy 203 ATTCGGGAGCATGGGTGAGTCAAGGAGGGCTTTCAGCTGCTCTGCGCAA 262
Db 121 ATTCGGGAGCATGGGTGAGTCAAGGAGGGCTTTCAGCTGCTCTGCGCAA 180

Qy 263 GACATTGCTTNTGATGCCAANAAA 289
Db 181 GACATTGCTTNTGATGCCAANAAA 207

RESULT 7
US-09-918-995-34259
; Sequence 34259, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918, 995
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 370
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO. 212
; LENGTH: 423
; TYPE: DNA
; ORGANISM: Bovine
; US-10-079-623-212

Query Match 27.3%; Score 127.8; DB 5; Length 423;
Best Local Similarity 72.5%; Pred. No. 2e-32; Mismatches 57; Indels 0; Gaps 0;

PRIOR APPLICATION NUMBER: US/10/225, 076
; PRIORITY FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 34259
; LENGTH: 425
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-918-995-34259

Query Match 25.1%; Score 117.6; DB 3; Length 425;
Best Local Similarity 77.7%; Pred. No. 5.7e-29;
Matches 146; Conservative 0; Mismatches 41; Indels 1; Gaps 1;
Db 281 GCGAAAGAACGAGCAGCTGAGTGTGACTGATGTCAGAATTCAGGC
Db 2 GCCATTAAGACAGCCGAGC-TGGTAGCGCCTGCAACTGAGCTTAACTC 60
Qy 341 ATCCTTNAAGCTGTCATNNCCGGGACTGNGACTGACCTGACCGGATATTGAGCT 400
Qy 61 ATCCTTCAAGCTGTCATCTCCAGGCTGCAAGCTGACCTGCTGAGCTTACCTG 120
Db 401 GGAGGCCCTGNTATGCTNCCCTCGCCTTACCTGATGCTGGCTGNGACCAAGTGGCAGCT 460
Db 121 GGTTTCTCTCTCCAGTGTCTGAGCTGACCTGCTGAGCTTACCTGCTGAGCT 180

RESULT 8
US-11-097-143-235b7
Sequence 2507, Application US/11097143
Publication No: US20050208558A1
GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
CURRENT APPLICATION NUMBER: US/11/097,143
CURRENt APPLICATION NUMBER: et al.
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
TITLE OF INVENTION: DRosOPHILA GENES.
FILE REFERENCE: CLO00728
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: 60/157,832
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: 60/160,191
PRIOR FILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR FILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/173,383
PRIOR FILING DATE: 1999-12-28
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR FILING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: 60/184,831
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 60/191,637
PRIOR FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 43008
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 2506
LENGTH: 4940
TYPE: DNA
ORGANISM: DROSOPHILA
US-11-097-143-2507

Query Match 19.9%; Score 93; DB 10; Length 4940;
Best Local Similarity 53.8%; Pred. No. 2.5e-20;
Matches 179; Conservative 0; Mismatches 153; Indels 1; Gaps 1;
Db 107 TCTGTGTTGANTCCGNAAGCTGTCAGNCAGCTGAGCTTACCTGAGCTA 166
Db 167 CTGTGTTGACCTTGATACTGACTCTGTGTCACATGNGACATGTCAG 226
Db 3019 GGTTCACCTTATGATCATCTACTGTGACGACGGCGTGGTAGACATGCGCAG 2360

RESULT 9
US-11-097-143-2306/c
sequence 2506, Application US/11097143
Publication No. US20050208558A1
GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
APPLICANT: et al.
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
TITLE OF INVENTION: DRosOPHILA GENES.
FILE REFERENCE: CLO00728
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: 60/157,832
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: 60/160,191
PRIOR FILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: US/11/097,143
PRIOR FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: 60/157,832
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: 60/160,191
PRIOR FILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: US/11/097,143
PRIOR FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: 60/157,832
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/173,383
PRIOR FILING DATE: 1999-12-28
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR FILING DATE: 2000-01-12
PRior APPLICATION NUMBER: 60/184,831
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 60/191,637
PRIOR FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 43008
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 2506
LENGTH: 4940
TYPE: DNA
ORGANISM: DROSOPHILA
US-11-097-143-2506

Query Match 19.9%; Score 93; DB 10; Length 4940;
Best Local Similarity 53.8%; Pred. No. 3.3e-20;
Matches 179; Conservative 0; Mismatches 153; Indels 1; Gaps 1;
Db 107 TCTGTGTTGANTCCGNAAGCTGTCAGNCAGCTGAGCTTACCTGAGCTA 166
Db 167 CTGTGTTGACCTTGATACTGACTCTGTGTCACATGNGACATGTCAG 226
Db 3019 GGTTCACCTTATGATCATCTACTGTGACGACGGCGTGGTAGACATGCGCAG 2360

RESULT 10
US-09-764-891-2676/c
Sequence 2676, Application US/09764891
; Publication No. US2003007780B1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 2676
; LENGTH: 283
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (65)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (141)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (275)
; OTHER INFORMATION: n equals a,t,g, or c
; US-09-764-891-2676

Query Match 15.8%; Score 74; DB 3; Length 283;
Best Local Similarity 77.6%; pred. No. 2,9e-14; Mismatches 97; Conservative 1; Indels 1; Gaps 1;
Matches 26;

Qy 242 TTCAAGCTCCCTGCTCCGGAGACATTTGCTTNTGATGCCAAAGAGCAGGCCAGGT 301
Db 219 TCTTGCCCCATGCCAGAAGCATTTGACCCATTAGAACGGCAGC-T 161
Qy 302 AGTCAGTCCTTGACTACTGATGTCAGAACGATTCAGGATTCCTTNAAGCTGCTATNN 361
Db 160 GGTTGAGGCCGCTTGAACAATNACGNGCAGGGTTAACGTCCTCAAGCTGCTTC 101
Qy 362 CCAGG 366
Db 100 CCAGG 96

RESULT 11
US-10-091-572-214/C
; Sequence 214, Application US/10091572
; Publication No. US20030054373A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA1881
; CURRENT APPLICATION NUMBER: US10/091,572
; CURRENT FILING DATE: 2002-03-07

PRIOR APPLICATION NUMBER: 09/764,850
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: 60/214,886
PRIOR FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: 60/217,487
PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/225,758
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/220,963
PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: 60/217,496
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/225,447
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: 60/218,290
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: 60/225,757
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/226,868
PRIOR FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: 60/216,647
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 60/225,267
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/216,880
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/225,274
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/231,869
PRIOR FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: 60/235,834
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: 60/225,274
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: 60/234,223
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: 60/228,924
PRIOR FILING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: 60/224,518
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/236,369
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/224,519
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/220,964
PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: 60/241,809
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/249,299
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/236,327
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/241,785
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/244,617
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 60/225,268
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/236,368
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/251,856
PRIOR FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: 60/251,868
PRIOR FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: 60/229,344
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/234,997
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: 60/229,343

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PRIORITY FILING DATE: 2000-09-01
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PRIORITY APPLICATION NUMBER: 60/229,287
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PRIORITY APPLICATION NUMBER: 60/229,513
PRIORITY FILING DATE: 2000-09-05
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PRIORITY APPLICATION NUMBER: 60/229,509
PRIORITY FILING DATE: 2000-09-05
PRIORITY APPLICATION NUMBER: 60/236,367
PRIORITY FILING DATE: 2000-09-29
PRIORITY APPLICATION NUMBER: 60/237,039
PRIORITY FILING DATE: 2000-10-02
PRIORITY APPLICATION NUMBER: 60/237,038
PRIORITY FILING DATE: 2000-10-02
PRIORITY APPLICATION NUMBER: 60/236,370
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PRIORITY FILING DATE: 2000-10-02
PRIORITY APPLICATION NUMBER: 60/237,037
PRIORITY FILING DATE: 2000-10-02
PRIORITY APPLICATION NUMBER: 60/237,040
PRIORITY FILING DATE: 2000-10-02
PRIORITY APPLICATION NUMBER: 60/240,960
PRIORITY FILING DATE: 2000-10-20
PRIORITY APPLICATION NUMBER: 60/239,935
PRIORITY FILING DATE: 2000-10-13
PRIORITY APPLICATION NUMBER: 60/239,937
PRIORITY FILING DATE: 2000-10-13
PRIORITY APPLICATION NUMBER: 60/241,787
PRIORITY FILING DATE: 2000-10-20
PRIORITY APPLICATION NUMBER: 60/245,474
PRIORITY FILING DATE: 2000-11-08
PRIORITY APPLICATION NUMBER: 60/246,532
PRIORITY FILING DATE: 2000-08-22
PRIORITY APPLICATION NUMBER: 60/249,216
PRIORITY FILING DATE: 2000-11-17
PRIORITY APPLICATION NUMBER: 60/249,210
PRIORITY FILING DATE: 2000-11-17
PRIORITY APPLICATION NUMBER: 60/226,681
PRIORITY FILING DATE: 2000-08-14
PRIORITY APPLICATION NUMBER: 60/225,759
PRIORITY FILING DATE: 2000-08-14
PRIORITY APPLICATION NUMBER: 60/225,213
PRIORITY FILING DATE: 2000-08-14
PRIORITY APPLICATION NUMBER: 60/227,182
PRIORITY FILING DATE: 2000-08-22
PRIORITY APPLICATION NUMBER: 60/225,214
PRIORITY FILING DATE: 2000-08-14
PRIORITY APPLICATION NUMBER: 60/235,836
PRIORITY FILING DATE: 2000-09-27
PRIORITY APPLICATION NUMBER: 60/230,438
PRIORITY FILING DATE: 2000-09-06
PRIORITY APPLICATION NUMBER: 60/215,135
PRIORITY FILING DATE: 2000-06-30
PRIORITY APPLICATION NUMBER: 60/225,266
PRIORITY FILING DATE: 2000-08-14
PRIORITY APPLICATION NUMBER: 60/249,218
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PRIORITY FILING DATE: 2000-11-17
PRIORITY APPLICATION NUMBER: 60/249,212
PRIORITY FILING DATE: 2000-11-17
PRIORITY APPLICATION NUMBER: 60/249,207
PRIORITY FILING DATE: 2000-11-17
PRIORITY APPLICATION NUMBER: 60/249,245
PRIORITY FILING DATE: 2000-11-17
PRIORITY APPLICATION NUMBER: 60/249,244
PRIORITY FILING DATE: 2000-11-17

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Query Match: Best Local Similarity: 15.8%; Score: 74; DB: 5; length: 283; Matches: 97; Conservative: 1; Mismatches: 26; Indels: 1; Gaps: 1;

Qy	242	TTCAGCTCCGCGCTGGCAAGACATTGCTTNTTGATGCCAAGAGCAGGCAGCGT	301
Db	219	TTCCTGCGCCCTGCGCAAGACATTGCTTGTGACCCAAAGAGCAGGGCGC-T	161
Qy	302	AGTAGCTCGCTTGACTACTGATGTCAGGAATTCAAGCATCTTNAAGTTGICATN	361
Db	160	GCTGAGCCGCTTGACAACTNAGTCAGGTTTAAGTCATCTTCAGCTTGTCATCTC	101
Qy	362	CCAGG 3' 66	
Db	100	CCAGG 96	

RESULT 12
US-10-264-237-718
Sequence: 718 Application US/10264237
Publication No. US2004009491A1
GENERAL INFORMATION:
APPLICANT: Birse et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA131P
CURRENT APPLICATION NUMBER: US/10/264,237

CURRENT FILING DATE: 2002-10-04
; PRIORITY APPLICATION NUMBER: PCT/US01/16450
; PRIORITY FILING DATE: 2001-05-18
; PRIORITY APPLICATION NUMBER: US 60/205,515
; PRIORITY FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SEQ ID NO: 718
; LENGTH: 574
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: misc_feature
; NAME/KEY: misc_feature
; LOCATION: (454)..(454)
; OTHER INFORMATION: n equals a,t,g, or c
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; NAME/KEY: misc_feature
; LOCATION: (523)..(523)
; OTHER INFORMATION: n equals a,t,g, or c

RESULT 13
; US-10-369-493-43142
; Sequence 43142, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIORITY APPLICATION NUMBER: US 60/360,039
; PRIORITY FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 43123
; SEQ ID NO: 43123
; LENGTH: 1773
; TYPE: DNA
; ORGANISM: Myxococcus xanthus

US-10-369-493-43142
; Query Match Score 51.8; DB 6; Length 1773;
; Best Local Similarity 44.0%; Pred. No. 2e-06;
; Matches 181; Conservative 0; Mismatches 229; Indels 1; Gaps 1;

Qy 53 CTGGCCAGTGTGGAGATGTCGCAAGTACACGAGGACCATGGGAGNTNCNTG 112
Db 196 CTGGCCTATCCCGCaccaTGccGacccTGccGacccTGccGacccTGccGaccc 255
Qy 113 TTTGAACTTCCNAAGTCANCGCCANCTCTCTACTGAGNGAGTTGGAGACTGTTG 172
Db 256 TATGGTGTGACCGGCTCGGATGTCGCGTGTGACCGTGCAGGCCATGCC 315
Qy 173 ACCTTGGATGACTTAGTGTCTGTCGCAATTGNGANGNACATGCCATGCG 232
Db 316 ATGGCCTGCGCATCTACCTCTCACCAACCGCGCGAACGCGTGTGCGGCTGCGC 375

RESULT 14
; US-10-369-493-43123
; Sequence 43123, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIORITY APPLICATION NUMBER: US 60/360,039
; PRIORITY FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 43123
; SEQ ID NO: 43123
; LENGTH: 1773
; TYPE: DNA
; ORGANISM: Myxococcus xanthus

US-10-369-493-43123
; Query Match Score 46.4; DB 6; Length 1773;
; Best Local Similarity 48.5%; Pred. No. 0.00013; Matches 127; Conservative 0; Mismatches 134; Indels 1; Gaps 1;

Qy 206 GNNGANCAGCATGCGCATGAGATGCGGAAGGCCCTTCAGCCTCTGCTCCGCGAAC 265
Db 301 GGTCGCGATTCGAGCCCTCGGGCGCTGTGATGCGACTTGCTGGAGCAGGAG 360
Qy 266 ATGGCTTNTGATGCCAAAGACAGGGAGGGTAGTGAGTGCGCTGACTGACTG 325
Db 361 ATCCGCTCTCTGCA-CMAGCACGCCATGGCGGCTCAGCAGCGGCTGTCACGAC 419
Qy 326 GCAAGATTCAGGCACTCTTNAAGCTCTCATTNCCAGGACTGAGCTNACCA 385
Db 420 CGCCCTCATCCAGGGCGGCTGAGCATGCCATCATGCTCCGACAGCAACAC 479
Qy 386 GGTGATGTTAGCTGGAGNCCTGNTATGCTCCTGCTGCTTACCTGATGCTGCC 445
Db 480 GTTGATGTTAGGGCTGGCTGCTGCTACACCTCGCCGGTGTGAGCTCGTCA 539

RESULT 15
; US-10-357-930-30101
; Sequence 30101, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert

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; APPLICANT: Brdege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; PRIOR REFERENCE: WPI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 30101
; LENGTH: 434
; ORGANISM: Homo sapiens
; US-10-357-930-30101

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Best Local Similarity 46.3%; Pred. No. 0; 0.00e9; Mismatches 160; Indels 1; Gaps 1;
Matches 139; Conservative 0; Mismatches 160; Indels 1; Gaps 1;
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Qy      140 CTGCTCTACTGAGCAGTTCAGGAGCTTGACCTTGATACTTAGTCCTGTGTCC 199
       |||||CGTTCTGGTGTGCCGGGTTGCTGGCTGSCACCGGGCGCTCTACATGGTGTCC
       |||||55 CTGTTCTGGTGTGCCGGGTTGCTGGCTGSCACCGGGCGCTCTACATGGTGTCC 114
Db      200 CACATTGNGANCNCATGCGCATGNCATGCGGAAGCGCCCTTTCACTCTGTGTCC 259
       |||||200 CACATTGNGANCNCATGCGCATGNCATGCGGAAGCGCCCTTTCACTCTGTGTCC 174
Qy      115 TGGCTGGCGGAGCGCGTGTACCGAGACATTGCGCAGCGGTCTACGCCAAGTGTGGCG 174
Db      260 CGAGACMTGCTTNTTGATGCCAAAAGCAGGGAGCGCTAGTGAGTGCCTGACTAC 319
       |||||260 CGAGACMTGCTTNTTGATGCCAAAAGCAGGGAGCGCTAGTGAGTGCCTGACTAC 233
Db      175 CAGAGCCCCGAAATCTTCTGAGAACCCCGCAC-GCGCGAACCTGCTGCGCCCTGACCAC 233
Qy      320 TGGTGTGGAAGATTCAAGGATCCTTNAAGCTGTGATINTTCAGGGACTTGCGCTG 379
Db      234 CGCACACACCCCTGATCAGAGCGTGTGGCACCGATCTGGCTGGCTGGCAACAC 293
       |||||234 CGCACACACCCCTGATCAGAGCGTGTGGCACCGATCTGGCTGGCTGGCAACAC 293
Qy      380 NAACCCAGGTGATGGTACCTGAGCTGAGNCCTTNTATCTGNCCTGCGCTTACCTGTAT 439
Db      294 GCTGCTGTTCTGGCGSCCTGTGATCTGCTGTCGTCGACCAAGCCGGCTGACTCCAT 353
       |||||294 GCTGCTGTTCTGGCGSCCTGTGATCTGCTGTCGTCGACCAAGCCGGCTGACTCCAT 353

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Search completed: January 20, 2006, 22:36:34
Job time : 659 secs

GenCore version 5.1.6
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Om nucleic - nucleic search, using sw model

Run on: January 20, 2006, 20:40:58 ; Search time 242 Seconds
(without alignments)

1594.049 Million cell updates/sec

Title: US-10-327-713-267

Perfect score: 468

Sequence: 1 gactgaggatggcccttagtg.....ngncacacccgcctcatgg 468

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 6049916 seqs, 41213615 residues

Total number of hits satisfying chosen parameters: 12099832

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA New,*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGNMENTS

Result No.	Score	Query Match Length	DB ID	Description
1	43.8	9.4	4990	US-11-128-061-932
2	43.8	9.4	4990	Sequence 932, App
3	37.8	8.1	2436	Sequence 932, App
4	37.8	8.1	2436	Sequence 368, App
5	36.6	7.8	198285	Sequence 368, App
6	36.2	7.7	201	Sequence 398, App
7	36.2	7.7	16175	Sequence 68215, A
8	35.2	7.5	201	Sequence 68215, A
9	35	7.5	2446	Sequence 68215, A
10	33.8	7.2	65455	Sequence 68215, A
11	33.6	7.2	5868	Sequence 68215, A
12	33.4	7.1	2548	Sequence 68215, A
13	33	7.1	1284	Sequence 68215, A
14	33	7.1	1284	Sequence 68215, A
15	32.8	7.0	1008	Sequence 68215, A
16	32.6	7.0	3321	Sequence 68215, A
17	32.2	6.9	201	Sequence 68215, A
18	32.2	6.9	201	Sequence 68215, A
19	32.2	6.9	201	Sequence 68215, A
20	32.2	6.9	201	Sequence 68215, A
21	32.2	6.9	503	Sequence 68215, A
22	32.2	6.9	4932	Sequence 68215, A

Query Match 9.4%; Score 43.8; DB 8; Length 4990;
Best Local Similarity 46.2%; Pred. No. 0.0017; Oy
Matches 108; Conservative 0; Mismatches 126; Indels 0; Gaps 0;

Sequence 59, Appl
Sequence 58, Appl
Sequence 1894, Ap
Sequence 1085, Ap
Sequence 2282, Ap
Sequence 579, Appl
Sequence 244, Appl
Sequence 7, Appl
Sequence 30, Appl
Sequence 29, Appl
Sequence 27, Appl
Sequence 1, Appl
Sequence 13414, A
Sequence 10, Appl
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Sequence 1893, Ap
Sequence 44073, A
Sequence 44073, A
Sequence 479, Appl
Sequence 112, Appl
Sequence 32, Appl
Sequence 58, Appl

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RESULT 2
US-11-128-049-932
; Sequence 932, Application US/11128049
; Publication No. US20060010513A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hahn, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
; TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METHODS FOR
; TITLE OF INVENTION: MAKING AND USING SAME
; FILE REFERENCE: 01997.027100
; CURRENT APPLICATION NUMBER: US 11/128,049
; CURRENT FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US 60/570,425
; PRIOR FILING DATE: 2004-05-11
; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 932
; LENGTH: 4990
; TYPE: DNA
; ORGANISM: Crictellus griseus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4986)..(4948)
; OTHER INFORMATION: n is a, c, g, or t
; US-11-128-049-932

Query Match          9.4%; Score 43.8; DB 8; Length 4990;
Best Local Similarity    46.2%; Pred. No. 0.0017; Gap 0;
Matches 108; Conservative 0; Mismatches 126; Indels 0; Gaps 0;
Db
Qy      5 GAGCTGGCCCTAGGTCGGCACTACTAGTGAAATGCGATCCCTTCTCTCTGGCGAGCTG 64
1407 GAGAGGCCCTGTATGTCCTCAAAGGTGAACGTGGACTCTGTGATTCCTGGACTTCGGG 1466
Qy      65 GTGGGAGATTGCGCAAGTAACGGGGCACATGGGAGNTNGTGTGTTGATGCCGN 124
1467 GTCTCTCCGGTCTCCAGGACAGTGGTCCCTCTGGCCAGGGTTCCCTGGTCCAG 1526
Qy      125 AAGCTCAGCNCANCTGCCTCTACTAGTGNACAGCTGCAAGCTGTGATCTGATC 184
Db
Qy      1527 GAAATACGGTCCAAAGGGTACCCCTGGAGAGACTGTATCCAAGGGGACAGGGCTTC 1586
Qy      185 CTAGTGCTGTGCCACATTGNNNANCATGCCATGNACATCGGAAGCC 238
Db
1587 CTGGGAACTGGCTTACGGAGGAGACTGGAGACCTGGAGCTGGAGAC 1640

RESULT 3
US-11-128-051-368
; Sequence 368, Application US/11128061
; Publication No. US20060003958A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hahn, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.

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; APPLICANT: Miller Christopher P.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
; FILE REFERENCE: 0197_027701
; CURRENT FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US 60/5570, 425
; PRIOR FILING DATE: 2004-05-11
; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: PatentIn version 3.3
SEQ ID NO 368
LENGTH: 2436
TYPE: DNA
ORGANISM: Mesocricetus auratus
FEATURE:
NAME/KEY: misc feature
LOCATION: (820)..(837)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (1541)..(1544)
OTHER INFORMATION: n is a, c, g, or t

Query Match
 Best Local Similarity 52.4%; Pred. No. 0.054; 48; Indels 0; Gaps 0;
 Matches 54; Conservative 1; Mismatches 1;

Qy 215 ATGCGCATCAGCAGGGAAAGCCCTTTCAGCTCCCTCTCCAGAACATGCTGTN 274
 Db 738 ATCAACCTCGGATAGGGAGGTTTCTCTCTGTGCACAGACTTGGTT 197

RESULT 5
 US-10-775-169-338
 ; Sequence 338, Application US/10775169
 ; Publication No. US20050287532A9
 ; General Information:
 ; APPLICANT: Wyeth
 ; APPLICANT: Burczynski, Michael
 ; APPLICANT: Trecichio, William
 ; APPLICANT: Twine, Natalie
 ; CURRENT APPLICATION NUMBER: US10/775,169
 ; TITLE OF INVENTION: Method for Monitoring Drug Activities In Vivo
 ; FILE REFERENCE: AW10080 (031896-01000)
 ; CURRENT FILING DATE: 2004-02-11
 ; NUMBER OF SEQ ID NOS: 5278
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO: 338
 ; LENGTH: 198285
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-775-169-338

Query Match 7.8%; Score 36.6; DB 7; Length 198285;
 Best Local Similarity 58.8%; Pred. No. 2.1;
 Matches 57; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
 Qy 198 CCCACATGNGNANGNCATGCCATCAGATGCCATCAGCTCC 257
 Db 118712 CCTACGACCATCTCCGATCACTCGGATCCGGAGCACCTTCTCCCTCTGC 118711

RESULT 6
 US-10-995-561-68215
 ; Sequence 68215, Application US/10995561
 ; Publication No. US20050272054A1
 ; General Information:
 ; APPLICANT: CARGILL, Michele et al.
 ; APPLICANT: CARGILL, Michele et al.
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 ; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
 ; TITLE OF INVENTION: DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001559
 ; CURRENT APPLICATION NUMBER: US/10/995,561
 ; CURRENT FILING DATE: 2004-11-24
 ; NUMBER OF SEQ ID NOS: 85702
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 68215
 ; LENGTH: 201
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-995-561-68215

Query Match 7.7%; Score 36.2; DB 7; Length 201;
 Best Local Similarity 57.7%; Pred. No. 0.085; 40; Indels 0; Gaps 0;
 Matches 56; Conservative 1; Mismatches 40;

Qy 198 CCCACATGNGNANGNCATGCCATCAGCTCC 257
 Db 118772 GCGAGGACCTCGGTTCTCCAGGAGACTAGACAG 118808

RESULT 7
 US-10-995-561-13399
 ; Sequence 13399, Application US/10995561
 ; Publication No. US20050272054A1
 ; General Information:
 ; APPLICANT: CARGILL, Michele et al.
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 ; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
 ; TITLE OF INVENTION: DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001559
 ; CURRENT APPLICATION NUMBER: US/10/995,561
 ; CURRENT FILING DATE: 2004-11-24
 ; NUMBER OF SEQ ID NOS: 85702
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 13399
 ; LENGTH: 16175
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-995-561-13399

Query Match 7.7%; Score 36.2; DB 7; Length 16175;
 Best Local Similarity 57.7%; Pred. No. 0.78; 40; Indels 0; Gaps 0;
 Matches 56; Conservative 1; Mismatches 40; Indels 0; Gaps 0;
 Qy 198 CCCACATGNGNANGNCATGCCATCAGCTCC 257
 Db 15156 CCTACACCATGTTCTGAATCACTTGCGGATCCGGAGCAGCTTCTCCCTCTGC 15215

Query Match 7.7%; Score 36.2; DB 7; Length 16175;
 Best Local Similarity 57.7%; Pred. No. 0.78; 40; Indels 0; Gaps 0;
 Matches 56; Conservative 1; Mismatches 40; Indels 0; Gaps 0;
 Qy 258 GGCAAGACATGCTTNTTGATGCCAAAGACGG 294
 Db 15216 GCAGAGACCTCGGTTCTCCAGGAGACTAGACAG 15252

RESULT 8
 US-10-995-561-68325
 ; Sequence 68325, Application US/10995561
 ; Publication No. US20050272054A1
 ; General Information:
 ; APPLICANT: CARGILL, Michele et al.
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 ; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
 ; TITLE OF INVENTION: DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001559
 ; CURRENT APPLICATION NUMBER: US/10/995,561
 ; CURRENT FILING DATE: 2004-11-24
 ; NUMBER OF SEQ ID NOS: 85702
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 68325
 ; LENGTH: 201
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-995-561-68325

Query Match 7.5%; Score 35.2; DB 7; Length 201;
 Best Local Similarity 62.7%; Pred. No. 0.18; 31; Indels 0; Gaps 0;
 Matches 52; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

Qy 212 CNCATGCCATCAGACATGCCGAAAGCCCTTTCAGCTCCCTGCTCGGAGACATGCT 271
 Db 8 CGATCAACTCGGATCCGGAGCACCTTCTCCCTCTGCGGAGACCTGGT 67

Query Match 7.7%; Score 36.2; DB 7; Length 201;
 Best Local Similarity 57.7%; Pred. No. 0.085; 40; Indels 0; Gaps 0;
 Matches 56; Conservative 1; Mismatches 40;

Qy 272 TTNTTGATGCCAAAGACGG 294
 Db 68 TCTTCCAGGAGACTAGACAG 90

RESULT 9
 US-11-136-527-3071
 ; Sequence 3071, Application US/11136527
 ; Publication No. US20050287570A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wyeth
 ; MOUNTS, William M
 ; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
 ; FILE REFERENCE: 031896-041000 (AM101086)
 ; CURRENT APPLICATION NUMBER: US/11/136,527
 ; CURRENT FILING DATE: 2005-05-25
 ; PRIORITY APPLICATION NUMBER: US 60/574,294
 ; PRIORITY FILING DATE: 2005-05-26
 ; NUMBER OF SEQ ID NOS: 362830
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 3071
 ; LENGTH: 2446
 ; TYPE: DNA
 ; ORGANISM: Rattus norvegicus
 ; US-11-136-527-3071

Query Match 7.5%; Score 35; DB 8; Length 2446;
 Best Local Similarity 62.4%; Pred. No. 0.72; Mismatches 0; Gaps 0;
 Matches 53; Conservative 0; Indels 0; Gaps 0;

QY 215 ATGGCCATGAGCATGGCGAAAGCCCTTTCAGCTCCTGCGCG3AAGACATTGCTTN 274
 Db 750 ATCAACACTGGCGATACCGAGAGCAGCTTCTCATCTTGTCGYAAGACTTGATTC 809

QY 275 TTGATGCCAAAGACAGGCAGC 299
 Db 810 TTCCAGGAGCCAAAGACAGG3AGC 834

RESULT 10
 US-11-124-368A-2884/C
 ; Sequence 2884, Application US/11124368A
 ; Publication No. US20050287559A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Michele Cargill
 ; ATTORNEY: James J. Devlin
 ; APPLICANT: May Luke
 ; TITLE OF INVENTION: Genetic Polymorphisms Associated with
 ; FILE REFERENCE: Vasculär Diseases, Methods of Detection and Uses Thereof
 ; CURRENT APPLICATION NUMBER: US/11/124,368A
 ; CURRENT FILING DATE: 2005-05-09
 ; PRIORITY APPLICATION NUMBER: US 60/568,845
 ; PRIORITY FILING DATE: 2004-05-07
 ; PRIORITY APPLICATION NUMBER: US 60/625,936
 ; NUMBER OF SEQ ID NOS: 2112
 ; SRID ID NO 2884
 ; LENGTH: 65455
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-11-124-368A-2884

Query Match 7.5%; Score 35; DB 8; Length 2446;
 Best Local Similarity 62.4%; Pred. No. 0.72; Mismatches 0; Gaps 0;
 Matches 53; Conservative 0; Indels 0; Gaps 0;

QY 215 ATGGCCATGAGCATGGCGAAAGCCCTTTCAGCTCCTGCGCG3AAGACATTGCTTN 274
 Db 750 ATCAACACTGGCGATACCGAGAGCAGCTTCTCATCTTGTCGYAAGACTTGATTC 809

QY 275 TTGATGCCAAAGACAGGCAGC 299
 Db 810 TTCCAGGAGCCAAAGACAGG3AGC 834

RESULT 11
 US-11-136-527-3354
 ; Sequence 3354, Application US/11136527
 ; Publication No. US20050287570A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wyeth
 ; MOUNTS, William M
 ; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
 ; FILE REFERENCE: 031896-041000 (AM101086)
 ; CURRENT APPLICATION NUMBER: US/11/136,527
 ; CURRENT FILING DATE: 2005-05-25
 ; PRIORITY APPLICATION NUMBER: US 60/574,294
 ; PRIORITY FILING DATE: 2005-05-26
 ; NUMBER OF SEQ ID NOS: 362830
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 3354
 ; LENGTH: 5868
 ; TYPE: DNA
 ; ORGANISM: Rattus norvegicus
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (5415)..(5416)
 ; OTHER INFORMATION: n is a, c, g, or t
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (5439)..(5439)
 ; OTHER INFORMATION: n is a, c, g, or t
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (5858)..(5858)
 ; OTHER INFORMATION: n is a, c, g, or t
 ; US-11-136-527-3354

Query Match 7.2%; Score 33.6; DB 8; Length 5868;
 Best Local Similarity 59.4%; Pred. No. 3.1; Mismatches 39; Indels 0; Gaps 0;
 Matches 57; Conservative 0; Gaps 0;

QY 8 CTGGCCCTTAGGTGGCGCACTGTGAATGTCAGATCCCCTGCTCTGGCCAGCTGGTG 67
 Db 1589 CTGGCGTCTGGCGAGCCCTGGCTGTGATGCGAAACACGCGCCCGCTGGTCCGCTGGTC 1648

QY 68 GAGATGTCGCCAAAGTAACAGGAGGACACATGGGG 103
 Db 1649 AGATGTCGCCCTGGACCCCGAGGTCTCCTGGAG 1684

RESULT 12
 US-11-136-527-2128
 ; Sequence 2128, Application US/11136527
 ; Publication No. US20050287570A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wyeth
 ; MOUNTS, William M
 ; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
 ; FILE REFERENCE: 031896-041000 (AM101086)
 ; CURRENT APPLICATION NUMBER: US/11/136,527
 ; CURRENT FILING DATE: 2005-05-25
 ; PRIORITY APPLICATION NUMBER: US 60/574,294
 ; PRIORITY FILING DATE: 2005-05-26
 ; NUMBER OF SEQ ID NOS: 362830
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 2128
 ; LENGTH: 2548
 ; TYPE: DNA
 ; ORGANISM: Rattus norvegicus
 ; US-11-136-527-2128

Query Match 7.1%; Score 33.4; DB 8; Length 2548;
 Best Local Similarity 49.6%; Pred. No. 2.4; Mismatches 65; Indels 0; Gaps 0;
 Matches 64; Conservative 0; Gaps 0;

QY 267 TGGCTTNTTGTGCGAAAGACAGGGCACGGTACTGAGTGTGACTGATGTT 326
 Db 10263 TTTTTTTTGTGGTAAAGCTCAGGGCACGGTACTGAGTGTGACTGATGTT 10204

QY 327 CAGAACATTCAGGCGATCC 344
 Db 10203 AAGAGCTGATAGAACCC 10186

QY 65 GTGGAGATGTCGCCAGTACCGAGGACACATGGGAGNTNTNTGANTCCCGN 124

1246 GTCGCTACTGTGCGCCATTACAGGCCAGGGAGCTTGTAGATTTGT 1325
 Qy |
 Db 125 AAGCTCAGNCANCCTCTACTGNAGCTAGNACTGACCTTGATAC 184
 ; Sequence 36207, Application US/10750185
 ; Publication No. US20050260603A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MMI GENOMICS, INC.
 ; APPLICANT: DENISE, Sue K.
 ; APPLICANT: KERR, Richard
 ; APPLICANT: ROSENFIELD, David
 ; APPLICANT: HOLM, Tom
 ; APPLICANT: BATES, Stephen
 ; APPLICANT: FANTIN, Dennis
 ; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
 ; FILE REFERENCE: MMII100-2
 ; CURRENT APPLICATION NUMBER: US/10/750,185
 ; PRIORITY FILING DATE: 2003-12-31
 ; PRIORITY APPLICATION NUMBER: US 60/437,482
 ; NUMBER OF SEQ ID NOS: 64922
 ; SOFTWARE: PatentIN version 3.1
 ; SEQ ID NO: 36207
 ; LENGTH: 1284
 ; TYPE: DNA
 ; ORGANISM: Bovine 19866881290303
 ; US-10-750-185-36207

RESULT 13
 US-10-750-185-36207/c
 Qy |
 Db 1326 CATCTGAGACCACTTCTAGAGACAGCTTCAAGGTTGTAATTAAAGCC 1385
 ; Sequence 36207, Application US/10750185
 ; Publication No. US20050260603A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MMI GENOMICS, INC.
 ; APPLICANT: DENISE, Sue K.
 ; APPLICANT: KERR, Richard
 ; APPLICANT: ROSENFIELD, David
 ; APPLICANT: HOLM, Tom
 ; APPLICANT: BATES, Stephen
 ; APPLICANT: FANTIN, Dennis
 ; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
 ; FILE REFERENCE: MMII100-2
 ; CURRENT APPLICATION NUMBER: US/10/750,185
 ; PRIORITY FILING DATE: 2003-12-31
 ; PRIORITY APPLICATION NUMBER: US 60/437,482
 ; NUMBER OF SEQ ID NOS: 64922
 ; SOFTWARE: PatentIN version 3.1
 ; SEQ ID NO: 36207
 ; LENGTH: 1284
 ; TYPE: DNA
 ; ORGANISM: Bovine 19866881290303
 ; US-10-750-185-36207

Query Match 7.1%; Score 33; DB 7; Length 1284;
 Best Local Similarity 50.7%; Pred. No. 2.2; Matches 72; Conservative 0; Mismatches 70; Indels 0; Gaps 0;
 Sequence 61, Application US/11055822
 Publication No. US20050260707A1
 GENERAL INFORMATION:
 APPLICANT: Pompejus, Markus
 APPLICANT: Kroger, Burkhard
 APPLICANT: Schroder, Hartwig
 APPLICANT: Zelder, Oskar
 APPLICANT: Haberhaeu, Gregor
 ; TITLE OF INVENTION: CORNYNEBACTERIUM GLUTAMICUM GENES ENCODING
 ; FILE REFERENCE: BGI-121CPN
 ; CURRENT APPLICATION NUMBER: US/11/055,822
 ; PRIORITY FILING DATE: 2005-02-11
 ; PRIORITY APPLICATION NUMBER: 09/605,740
 ; PRIORITY FILING DATE: 2000-06-23
 ; PRIORITY APPLICATION NUMBER: 60/141,031
 ; PRIORITY FILING DATE: 1999-06-25
 ; PRIORITY APPLICATION NUMBER: 60/142,101
 ; PRIORITY FILING DATE: 1999-07-02
 ; PRIORITY APPLICATION NUMBER: 60/143,613
 ; PRIORITY FILING DATE: 1999-08-12
 ; PRIORITY APPLICATION NUMBER: 60/187,970
 ; PRIORITY FILING DATE: 2000-03-09
 ; PRIORITY APPLICATION NUMBER: DE 19930476.9
 ; PRIORITY FILING DATE: 1999-07-01
 ; PRIORITY APPLICATION NUMBER: DE 19931415.2
 ; PRIORITY FILING DATE: 1999-07-08
 ; PRIORITY APPLICATION NUMBER: DE 19931418.7
 ; PRIORITY FILING DATE: 1999-07-08
 ; PRIORITY APPLICATION NUMBER: DE 19931419.5
 ; PRIORITY FILING DATE: 1999-07-08
 ; PRIORITY APPLICATION NUMBER: DE 19931420.9
 ; PRIORITY FILING DATE: 1999-07-08
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 1158
 ; SEQ ID NO: 61
 ; LENGTH: 1008
 ; TYPE: DNA
 ; ORGANISM: Corynebacterium glutamicum
 ; NAME/KEY: CDS
 ; FEATURE: CDS
 ; LOCATION: (101)..(985)
 ; OTHER INFORMATION: RKC00733
 ; US-11-055-822-61

Query Match 7.0%; Score 32.8; DB 8; Length 1008;
 Best Local Similarity 45.3%; Pred. No. 2.3;

Matches	91; Conservative	0;	M. matches	110; Indels	0;	Gaps	0;
Qy	268	TGCTTINTTGATGCCAAGAACGGACCGTAGTGAGCGCTGACTGTGTC					327
Db	609	TGAGCTATTGATCCATCAACGCTGATCTCTTACCGCTGACGATGTC					668
Qy	328	AAGAATCAGGCATCTTNAAGCTGTCATNTNCAGGGACTGNCOAGTGACCCAGG					387
Db	669	ATAATATGGCTAACCTGCAACACTTCTCACGGCATCTCCCTACTTGACCC					728
Qy	388	TGATTTGCTAGCTGGAGNCCCTGNNPATGCTGTCNCCTCGCTTACCTGATGCTG					447
Db	729	TATCGGGTGTGGTATGAGTTATCATCTCCCACTCICGACTCGTGGCTGG					788
Qy	448	NNNNACACGCCCTCATGG	468				
Db	789	TATCCATTCCTCACCATCG	809				

Search completed: January 20, 2006, 22:40:43
 Job time : 245 secs